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Gly Tyr Gln Asn Pro Ala Pro Phe Ser Ile Asn Gln Ser Gln Thr Val
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Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile Glu Glu Leu
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Leu Val Glu Arg Thr Gly Ala Pro Phe Cys Ser Pro Thr Ser Ser Gly
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Trp Arg Arg Ser Arg Ala Ser Ala Ile Ala Ala Gly Val His Pro Gln
           ' 85
                                    90
Asp Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu
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                               105
Lys Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr
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Phe Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro
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Leu His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr
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Leu Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg
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Lys Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln
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Ile Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp
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                                             60
Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile
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Leu Lys Asp Lys Lys Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His
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                                     90
Pro Gln Asn Tyr Phe Lys Tyr Thr Glu Lys His Lys Glu Met Leu Pro
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                            120
Pro Tyr Lys
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7

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Pro Thr Leu Val Gln Thr Gly Leu His Gly Arg His Ile Leu Gly Arg
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His Val Phe Gly Ser Ala Ala Asn Leu Phe Ser Cys Ala Ile Asp Gln
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Val Phe Pro Asn Glu Gly Cys Leu Pro Tyr Ser Cys Gln Glu Pro Asn
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Tyr Ala Asp His Asn Tyr Gly Ala Arg Pro Pro Pro Thr Pro Pro Ala
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Ser Pro Pro Pro Ser Val Leu Ile Ser Lys Asn Glu Val Gly Ile Phe
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Thr Thr Pro Asn Phe Asp Glu Thr Ser Ser Ala Thr Thr Ile Ser Thr
Ser Glu Asp Gly Ser Tyr Gly Thr Asp Val Thr Arg Cys Ile Cys Gly
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Phe Thr His Asp Asp Gly Tyr Met Ile Cys Cys Asp Lys Cys Ser Val
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Trp Gln His Ile Asp Cys Met Gly Ile Asp Arg Gln His Ile Pro Asp
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Thr Tyr Leu Cys Glu Arg Cys Gln Pro Arg Asn Leu Asp Lys Glu Arg
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                    150
Ala Val Leu Leu Gln Arg Arg Lys Arg Glu Asn Met Ser Asp Gly Asp
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Thr Ser Ala Thr Glu Ser Gly Asp Glu Val Pro Val Glu Leu Tyr Thr
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Ala Phe Gln His Thr Pro Thr Ser Ile Thr Leu Thr Ala Ser Arg Val
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Ser Lys Val Asn Asp Lys Arg Lys Lys Ser Gly Glu Lys Glu Gln
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His Ile Ser Lys Cys Lys Lys Ala Phe Arg Glu Gly Ser Arg Lys Ser
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Ser Arg Val Lys Gly Ser Ala Pro Glu Ile Asp Pro Ser Ser Asp Gly
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Ser Asn Phe Gly Trp Glu Thr Lys Ile Lys Ala Trp Met Asp Arg Tyr
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Glu Glu Ala Asn Asn Gln Tyr Ser Glu Gly Val Gln Arg Glu Ala
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Gln Arg Ile Ala Leu Arg Leu Gly Asn Gly Asn Asp Lys Lys Glu Met
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300

315

295

310

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Leu Pro Pro Asp Ala Leu Ile Ile Glu Tyr Arg Gly Lys Phe Met Leu
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Arg Glu Gln Phe Glu Ala Asn Gly Tyr Phe Phe Lys Arg Pro Tyr Pro
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Phe Val Leu Phe Tyr Ser Lys Phe His Gly Leu Glu Met Cys Val Asp
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Ala Arg Thr Phe Gly Asn Glu Ala Arg Phe Ile Arg Arg Ser Cys Thr
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Pro Asn Ala Glu Val Arg His Glu Ile Gln Asp Gly Thr Ile His Leu
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Tyr Ile Tyr Ser Ile His Ser Ile Pro Lys Gly Thr Glu Ile Thr Ile
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Ala Phe Asp Phe Asp Tyr Gly Asn Cys Lys Tyr Lys Val Asp Cys Ala
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Cys Leu Lys Glu Asn Pro Glu Cys Pro Val Leu Lys Arg Ser Ser Glu
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Ser Met Glu Asn Ile Asn Ser Gly Tyr Glu Thr Arg Arg Lys Lys Gly
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Lys Lys Asp Lys Asp Ile Ser Lys Glu Lys Asp Thr Gln Asn Gln Asn
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Ile Thr Leu Asp Cys Glu Gly Thr Thr Asn Lys Met Lys Ser Pro Glu
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Thr Lys Gln Arg Lys Leu Ser Pro Leu Arg Leu Ser Val Ser Asn Asn
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Gln Glu Pro Asp Phe Ile Asp Asp Ile Glu Glu Lys Thr Pro Ile Ser
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Asn Glu Val Glu Met Glu Ser Glu Glu Gln Ile Ala Glu Arg Lys Arg
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Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
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Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
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Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
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Val Thr Ser Gly Leu Thr Tyr Ile Lys Ile Gln Leu Val Lys Ala Glu
Val Ala Ser Ala Val Cys Leu Arg Leu His Arg Pro Arg Asp Ala Ser
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				85					90					95	e Gly
Thr	Thi	r Sei	r Sei 100		a Thr	· Val	l Asr	Ası 109		o Phe	e Leu	ı Pro	Ser 110		ı Asp
Glr	ı Val	l Se:		s Thi	Ser	: Ile	e Gly 120		) Let	ı Arç	J Lev	Leu 125		His	Cys
Leu	130	His	s Ile	e Sei	Asp	Lev 135		Gl	/ Met	Met	Ala 140	Ser		a Ala	Ala
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Arg	Asn	Cys	Ala		Ser	Gly	Ser 200	Asp		Thr	Asp		Asn		Pro
Leu	Leu 210	Phe		' Arģ	Leu	Asn 215	Gly		Ser	Ser	Asp 220			Ile	Asp
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Asp 385	Asp	Ser	Lys	Asn	Ala 390	Gln	Ala	Pro	Leu	Ala 395		Thr	Glu	Ser	His 400
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Ser	Glu	Val	Asn		Leu	Trp	Thr	Ala		Leu	Phe	Leu	Leu		His

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Cys	Ile	Ser	Cys		Pro	Asn	Asn	Gln	_		Met	Ala	Gln		Leu
_			-1-	565	<b></b>			<b>~3</b> -	570		•	<b>.</b>	D	575	<b>7</b>
Cys	GIU	Leu	580	Gin	Thr	ser	Pro	585	Arg	GIA	ASD	Leu	590		Ser
Glv	Acn	Tla		Glv	Dhe	Tla	Ara		T.011	Dhe	T.e.11	Gla			Leu
Q. y	7311	595		G <sub>2</sub> y		***	600	****	200		200	605			
Glu	Asp			Val	Thr	Met		Leu	Gln	Ser	Pro			Leu	Tyr
	610		-			615					620				-
Lys	Gly	Arg	Ile	Asn	Ala	Thr	Ser	His	Val	Ile	Gln	His	Pro	Met	Tyr
625					630					635					640
Gly	Ala	Gly	His	_	Phe	Arg	Thr	Leu		Leu	Pro	Val	Ser		Thr
_	_	_		645	_	_		_	650		_	_	-1.	655	
Leu	ser	Asp		Leu	Asp	Arg	Vai		Asp	Thr	Pro	Ser	11e	Thr	Ala
T	T 011	710	660	Glu	Cln	Larg	700	665	Tuc	G1.	Lve	Lvc	-	uic	Glu
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705					710					715					720
Ala	Thr	Pro	Pro		Pro	Pro	Ser	Arg		Gly	Arg	Thr	Ile		Asp
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Lys	Iie	GIY		Thr	Ser	GIY	Ala		Ala	Ala	Asn	rys	750	ile	Thr
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Arg	Leu	HIS	820	GIU	Lys	Asp		825	_	Leu	Leu		ser 830	Cys	Pro
Glu	) en	Glu		T.011	Thr	Pro		_		Cys	Met			716	T.411
GIU	ASP	835	n.a	TC G		- 10	840	nop	O.L.	Cys	Mec	845	<b>-</b> 1	110	Deu
Asp	Glu	_	Leu	Leu	Glu	Thr		Pro	Ile	Gln	Ser		Leu	Gln	Val
	850					855	- 2				860				
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T1 -	C1	<b>~1</b> -	900	<b>01</b>	G3	T 0	17- 1	905	c1	71-	Des	<b>C1</b>	910	17 n 1	N 1 -
TIE	GIU	915	ser	GIA	GIU	ьeu	920	TÅL	GIU	Ala	FLO	925	TIIT	AUT	wrg
A]a	G] 11		Pro	Pro	Ile	Lvs		Ala	Val	Gln	Thr		Ser	Pro	Ile
						_, _									

020				025					040				
930				935	<b>5</b> 2-	<b>61</b>	•	<b>D</b> b -	940		•	D	G]
Pro Ala H	is Ser	Leu		Ala	Pne	GIY	Leu		Leu	Arg	ьeu	Pro	
945		_	950	_			_	955			_		960
Tyr Ala G	lu vai		Leu	Lys	GIU	Arg	_	Hls	Ата	GIn	Cys		Leu
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Cys Leu S	er Ala	Leu	Ser	His	His	Ser	Pro	Arg	Val	Pro	Asn	Ser	Ser
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Val Asn G	ln Thr	Glu	Pro	Gln	Val	Ser	Ser	Ser	His	Asn	Pro	Thr	Ser
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Thr Glu G			T.eu	Tvr	Tro			Glv	Thr	Glv			Thr
	)75			-1-	1080		2,5	OL,		1085		<b>-</b> 1	****
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Arg Leu G	63	C2	uio			Cura	T 011	T 011			T ou	- ו מ	C ~ ~
-	tu Giu	GIU			1111	Cys	neu			vai	Leu	MIG	1120
1105	B	**- 7	1110		*1-	17- 3	•	1115			<b>01</b> -		
Tyr Ile A	sn Pro			ser	Ala	vaı			GIU	Ala	GIN		
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His Glu T	_	_	GIn	Asn	ser			Leu	Pro	Ser			Leu
_	114	0				1145	•				1150	)	
			_	_			_			_	_	_	_
Glu Leu L		Gln	Ser	Cys			Pro	Ala	Met			Tyr	Leu
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1400

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Phe Gly Cys Val Asn Ala Ile Glu Phe Ser Asn Asn Gly Gly Gln Trp
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Leu Val Ser Gly Gly Asp Asp Arg Arg Val Leu Leu Trp His Met Glu
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Gln Ala Ile His Ser Arg Val Lys Pro Ile Gln Leu Lys Gly Glu His
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His Ser Asn Ile Phe Cys Leu Ala Phe Asn Ser Gly Asn Thr Lys Val
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Ala Val Lys Phe Arg Asp Lys Glu Trp Ile Arg Pro Asp Lys Tyr Gly
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545				204	550		0111	_,,	_, _	555	-1-	_,_		472	560
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GIU	د رت	110	Lys	565	GIU	1100	AJII	014	570		001	****		575	<b>-</b> y 5
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GIU	פעם	GIII	580	_	110		درد	585	כנם	GIU	non	204	590	1123	****
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Thr	Thr		λen	Cve	Δτα	Dhe		Larg	Δτα	Tare	Tle		Tle	Lys	Ara
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Thr	7 ~~	Glu	T.e.ii		ጥሙ	Δνα	Gln	1.011		Thr	T.em	Gln	Live	Leu	Δνα
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C1		λ <b>~~</b>	Cln	Cln	Dro		7000	T 033	Taro	<b>71</b> -		Clu	Mot	Gln	TIA
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	T	~1×										T + + G	Cln	T	
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Ala	Leu	ьys		HIS	GIII	ren	GIU		Int	PIO	гåг	ASII		His	ьys
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Ala	Tle	ጥህን			Δνα	T.ou	ב ז ת			T 011	Dane	C1			Leu
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 Asn Ile Gln Asn Ile Asp Glu Asp Glu Asp Leu Glu Val Phe Arg Asn
 Ser Leu Tyr Ala Pro Asp Tyr Ser Ser Arg Leu Asp Ile Val Arg Ala
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Asn Ser Lys Ser Pro Leu Gln Arg Ser Leu Ser Ala Lys Cys Val Ser
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Gly Thr Gly Gln Val Ser Thr Cys Arg Leu Arg Lys Asp Gln Gln Ala
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Ala Pro Pro Pro Ile Ser Pro Val Leu Pro Leu Val Pro Pro Pro Ala
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Thr Ala Leu Asn Pro Pro Ala Pro Pro Thr Phe His Gln Pro Gln Lys
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Phe Ala Gly Val Asn Lys Ala Pro Ser Val Ile Thr His Thr Ala Ser
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Ala Thr Leu Thr His Asp Ala Pro Ala Thr Thr Phe Ser Gln Ser Gln
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Gly Leu Val Ile Thr Thr His His Pro Ala Pro Ser Ala Ala Pro Cys
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Gly Leu Ala Leu Ser Pro Val Thr Arg Pro Pro Gln Pro Arg Leu Thr
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Phe Val His Pro Lys Pro Val Ser Leu Thr Gly Gly Arg Pro Lys Gln
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Pro His Lys Ile Val Pro Ala Pro Lys Pro Glu Pro Val Ser Leu Val
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Leu Lys Asn Ala Arg Ile Ala Pro Ala Ala Phe Ser Gly Gln Pro Gln
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Ala Val Ile Met Thr Ser Gly Pro Leu Lys Arg Glu Gly Met Leu Ala
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Ser Thr Val Ser Gln Ser Asn Val Val Ile Ala Pro Ala Ala Ile Ala
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Arg Ala Pro Gly Val Pro Glu Phe His Ser Ser Ile Leu Val Thr Asp
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Lys Arg Arg Phe Asn Ile Lys Met Cys Phe Asp Met Leu Asn Ser Leu
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Ile Ser Asn Asn Ser Lys Leu Thr Ser His Ala Ile Thr Leu Gln Lys
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Thr Val Glu Tyr Ile Thr Lys Leu Gln Gln Glu Arg Gly Gln Met Gln
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Glu Glu Ala Arg Arg Leu Arg Glu Glu Ile Glu Glu Leu Asn Ala Thr
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Arg Arg Gln Phe Asp His Met Lys Asp Met Phe Asp Glu Tyr Val Lys
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Thr Arg Thr Leu Gln Asn Trp Lys Phe Trp Ile Phe Ser Ile Ile Ile
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Lys Pro Leu Phe Glu Ser Phe Lys Gly Met Val Ser Thr Ser Ser Leu
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Leu Pro Ile Leu Arg Pro Met Val Leu Ser Thr Leu Arg Gln Leu Ser
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Phe Leu Met Glu Asn Arg Val Gln Ser Phe Tyr Gln Gln Glu Leu Glu
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Met Val Glu Ser Leu Leu Ser Leu Ala Asn Gln Pro Val Ile His Ser
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Ala Cys Ser Asp Gln Val Asn Phe Lys Lys Asp Thr Thr Ser Lys Ala
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Ile His Ser Ile Phe Lys Asn Ala Ile Gln Leu Leu Gln Glu Lys Gly
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Asp Cys Gln Lys Pro Asn His Met Glu Lys Gly Cys His Phe Leu His
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Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg Pro Gly Leu Ser Glu Ala
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Val Leu Gln Gln Val Leu Glu Leu Glu Asp Gln Ser Asp Ile Val
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Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
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  Lys Glu Pro Leu Gly Arg Ala Glu Arg Pro Gly Arg Pro Cys Thr Arg
  Leu Gln Pro Ala Gly Ser Val Ser Ser Thr Pro Leu Ser Thr Pro Cys
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  Ser Ser Val Pro Ser Ser Pro Ser Phe Ser Pro Thr Glu Gln Lys Thr
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                                          75
  His Leu Glu Asp Leu Tyr Trp Met Ala Ser Asn Tyr Gln Gln Met Asn
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  Pro Glu Ala Leu Asn Leu Thr Pro Glu Asp Ala Val Glu Ala Leu Ile
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 Gly Ser His Pro Val Pro Gln Pro Leu Gln Ser Phe Asp Ser Phe Arg
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Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln
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Ser Leu Phe Glu Glu Ala His Lys Met Val Arg Glu Ala Asn Met Lys
Gln Ala Ala Ser Glu Lys Gln Leu Lys Glu Ala Arg Gly Lys Ile Asp
Met Leu Gln Ala Glu Val Thr Ala Leu Lys Thr Leu Val Ile Thr Ser
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Thr Pro Ala Ser Pro Asn Arg Glu Leu His Pro Gln Leu Leu Ser Pro
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Thr Lys Ala Gly Pro Arg Lys Gly His Ser Arg His Lys Ser Thr Ser
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Ser Thr Leu Cys Pro Ala Val Cys Pro Ala Ala Gly His Thr Leu Thr
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Glu Val Asp Cys Ser Ser Thr Asn Thr Cys Ala Leu Ser Gly Leu Thr
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Tyr His Pro Thr Pro Ser Gln Thr Arg Leu Ala Thr Gln Leu Thr Glu
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Glu Glu Gln Ile Arg Ile Ala Gln Arg Ile Gly Leu Ile Gln His Leu
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Pro Leu Val Pro Leu Arg Ser Leu Gly Leu Ser Leu Ser Gly Gly Asp
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Gln Glu Asp Ala Gly Arg Ile Leu Ile Glu Glu Leu Arg Asp Arg Phe
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Pro Tyr Leu Ser Glu Ser Tyr Leu Ile Thr Thr Asp Ala Ala Gly Ser
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Ile Ala Thr Ala Thr Pro Asp Gly Gly Val Val Leu Ile Ser Gly Thr
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Gly Ser Asn Cys Arg Leu Ile Asn Pro Asp Gly Ser Glu Ser Gly Cys
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Gly Gly Trp Gly His Met Met Gly Asp Glu Gly Ser Ala Leu Ser Ala
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                                        235
Pro Ser Ala Tyr Trp Ile Ala His Gln Ala Val Lys Ile Val Phe Asp
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Ser Ile Asp Asn Leu Glu Ala Ala Pro His Asp Ile Gly Tyr Val Lys
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Gln Ala Met Phe His Tyr Phe Gln Val Pro Asp Arg Leu Gly Ile Leu
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Thr His Leu Tyr Arg Asp Phe Asp Lys Cys Arg Phe Ala Gly Phe Cys
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                                            300
Arg Lys Ile Ala Glu Gly Ala Gln Gln Gly Asp Pro Leu Ser Arg Tyr
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Ile Phe Arg Lys Ala Gly Glu Met Leu Gly Arg His Ile Val Ala Val
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                                   330
Leu Pro Glu Ile Asp Pro Val Leu Phe Gln Gly Lys Ile Gly Leu Pro
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Ile Leu Cys Val Gly Ser Val Trp Lys Ser Trp Glu Leu Leu Lys Glu
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Gly Phe Leu Leu Ala Leu Thr Gln Gly Arg Glu Ile Gln Ala Gln Asn
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                                           380
Phe Phe Ser Ser Phe Thr Leu Met Lys Leu Arg His Ser Ser Ala Leu
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                                       395
Gly Gly Ala Ser Leu Gly Ala Arg His Ile Gly His Leu Leu Pro Met
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Asp Tyr Ser Ala Asn Ala Ile Ala Phe Tyr Ser Tyr Thr Phe Ser
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                            40
Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val
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                                             60
Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys Pro Glu
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Ile Gln Gln Glu Leu Ile Asn Gln Gly Leu
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90
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Ile Thr Asp Arg Tyr Lys Asn Leu Pro Thr Ala Ser Arg Lys Leu Gln
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                                                125
Phe Leu Glu Leu Gln Lys Asp Leu Val Asp Asp Phe Arg Ile Arg Leu
                        135
Thr Gln Val Met Lys Glu Glu Thr Arg Ala Ser Leu Gly Phe Arg Tyr
                                        155
145
Cys Ala Ile Leu Asn Ala Val Asn Tyr Ile Ser Thr Val Leu Ala Asp
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                165
Trp Ala Asp Asn Val Phe Phe Leu Gln Leu Gln Gln Ala Ala Leu Glu
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            180
Val Phe Ala Glu Asn Asn Thr Leu Ser Lys Leu Gln Leu Gly Gln Leu
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Ala Ser Met Glu Ser Ser Val Phe Asp Asp Met Ile Asn Leu Leu Glu
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Gln Ile Arg Asp Ile Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val
                            40
                                                45
Lys Asp Ala Ala Lys Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala
Lys Glu Met Ile Arg Ser Arg Lys Ala Val Ser Lys Leu Tyr Ala Ser
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Lys Ala His Met Asn Ser Val Leu Met Gly Met Lys Asn Gln Leu Ala
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Val Leu Arg Val Ala Gly Ser Leu Gln Lys Ser Thr Glu Val Met Lys
                                105
Ala Met Gln Ser Leu Val Lys Ile Pro Glu Ile Gln Ala Thr Met Arg
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Glu Leu Ser Lys Glu Met Met Lys Ala Gly Ile Ile Glu Glu Met Leu
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                                            140
Glu Asp Thr Phe Glu Ser Met Asp Asp Gln Glu Glu Met Glu Glu Glu
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Ala Glu Met Glu Ile Asp Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala
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Leu Gly Lys Ala Pro Ser Lys Val Thr Asp Ala Leu Pro Glu Pro Glu
                                185
Pro Pro Gly Ala Met Ala Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu
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Ala Leu Glu Ala Met Gln Ser Arg Leu Ala Thr Leu Arg Ser
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Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys Leu Val Gly Ser Pro
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Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu Glu Arg Met Arg Asn
                            40
Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln Ala Gly Ser Ser Gly
                        55
Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val Met Glu Glu
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Glu Trp Asn Ala Leu Gln Xaa Gln Trp Xaa Asn Cys Pro Glu Asp Leu
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95
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Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu Glu Glu Ile Gln
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Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser Glu Tyr Glu Lys
                           120
                                              125
Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met Leu Ala Glu Trp
                                          140
                       135
Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys Tyr Asn Leu Arg
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Ile Thr Ser Gly Val Val Cys Gln Cys Gly Leu Ser Ile Pro Ser
                                  170
               165
His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala Cys Leu Glu Gly
                               185
Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr Pro Glu Phe Ser
                           200
Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu Met Ser Cys Leu
                                          220
Ala Cys Asp Thr Trp Ala Val Ile Leu
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 aatgtgtgcc agaagactcg ggaggaccag ggaagcaaag cccttctgga actacaagca
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tgcaggaggt ccaaaaggat ggaatgattt aggaaatcct agcaaatgaa aatgtgtggg
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ctttcc
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                                25
                                                    30
Gly Thr Ser Ser Leu Ile Ser Gly Leu Ile Leu Ile Phe Glu Trp Trp
        35
                            40
Tyr Phe Arg Lys Tyr Gly Thr Ser Phe Ile Glu Gln Val Ser Val Ser
                        55
His Leu Arg Pro Leu Leu Gly Gly Val Asp Asn Asn Ser Ser Asn Asn
Ser Asn Ser Ser Asn Gly Asp Ser Asp Ser Asn Arg Gln Ser Val Ser
                                    90
                85
Glu Cys Lys Val Trp Arg Asn Pro Leu Asn Leu Phe Arg Gly Ala Glu
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105
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Tyr Asn Arg Tyr Thr Trp Val Thr Gly Arg Glu Pro Leu Thr Tyr Tyr
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Asp Met Asn Leu Ser Ala Gln Asp His Gln Thr Phe Phe Thr Cys Asp
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                    135
Ser Asp His Leu Arg Pro Ala Asp Ala Ile Met Gln Lys Ala Trp Arg
                                   155
                 150
Glu Arg Asn Pro Gln Ala Arg Ile Ser Ala Ala His Glu Ala Leu Glu
                                170
              165
Ile Asn Glu Thr Arg His Gln Cys Leu Gly Val His Gln Lys Lys Ala
                            185
Ser Asn Val Cys Gln Lys Thr Arg Glu Asp Gln Gly Ser Lys Ala Leu
                         200
Leu Glu Leu Gln Ala Tyr Ala Asp Val Gln Ala Val Leu Ala Lys Tyr
                      215
Asp Asp Ile Ser Leu Pro Lys Ser Ala Thr Ile Cys Tyr Thr Ala Ala
                                 235
                 230
Leu Leu Lys Ala Arg Ala Val Ser Asp Lys Phe Ser Pro Glu Ala Ala
              245 250
Ser Arg Arg Gly Leu Ser Thr Ala Glu Met Asn Ala Val Glu Ala Ile
          260
                            265
His Arg Ala Val Glu Phe Asn Pro His Val Pro Lys Tyr Leu Leu Glu
               280
Met Lys Ser Leu Ile Leu Pro Pro Glu His Ile Leu Lys Arg Gly Asp
                    295
Ser Glu Ala Ile Ala Tyr Ala Phe Phe His Leu Ala His Trp Lys Arg
                  310
                                    315
Val Glu Gly Ala Leu Asn Leu Leu His Cys Thr Trp Glu Gly Thr Phe
                                330
              325
Arg Met Ile Pro Tyr Pro Leu Glu Lys Gly His Leu Phe Tyr Pro Tyr
                             345
           340
Pro Ile Cys Thr Glu Thr Ala Asp Arg Glu Leu Leu Pro Ser Phe His
                        360
Glu Val Ser Val Tyr Pro Lys Lys Glu Leu Pro Phe Phe Ile Leu Phe
                                        380
                      375
Thr Ala Gly Leu Cys Ser Phe Thr Ala Met Leu Ala Leu Leu Thr His
                                     395
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Gln Phe Pro Glu Leu Met Gly Val Phe Ala Lys Ala Val Ser Val Cys
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attgagaaga tootgagoga ggaccoogg tggcaagatg ccaacttogt getgggcago

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Gly Val Leu Ala Ser Gln Ala Met Ile Glu Lys Ile Leu Ser Glu Asp
Pro Arg Trp Gln Asp Ala Asn Phe Val Leu Gly Ser Tyr Lys Thr Glu
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Gln Cys Pro Lys Pro Pro Arg Leu Cys Arg Gln Gly Tyr Ala Cys Pro
                                         75
                    70
His Tyr His Asn Ser Arg Asp Arg Arg Arg Asn Pro Arg Arg Phe Gln
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Tyr Arg Ser Thr Pro Cys Pro Ser Val Lys His Gly Asp Glu Trp Gly
                                 105
Glu Pro Ser Arg Cys Asp Gly Gly Asp Gly Cys Gln Tyr Cys His Ser
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Tyr Met Gln Gly Leu Ser Ala Cys Glu Gln Ile Arg Ala Ala Leu Tyr
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Arg Glu Glu Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe
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Gly Gly Thr Glu Thr Thr Ser Met Leu Xaa Val Pro Gly Val Thr Gln
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Ile Leu Leu Glu Ala Gly Pro Lys Lys Val Leu Glu Lys Leu Ser
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Glu Thr Tyr Ser Asn Arg Val Ser Ser Ile Ser Pro Gly Ser Ala Thr
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Leu Leu Ser Ser Phe Gly Ala Trp Asp His Ile Cys Asn Met Arg Tyr
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Arg Ala Phe Arg Arg Met Gln Val Trp Asp Ala Cys Ser Glu Ala Leu
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Asp Arg Val Thr Val Leu Tyr Arg Ser Lys Ala Ile Arg Tyr Thr Trp
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Pro Cys Pro Phe Pro Met Ala Asp Ser Ser Pro Trp Val His Ile Thr
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Leu Gly Asp Gly Ser Thr Phe Gln Thr Lys Leu Leu Ile Gly Ala Asp
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His Gly Gly Thr Cys Ser Arg Gln Glu Leu Gly Val Ser Asp Val Leu
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Gly Tyr Val His Pro Asp Leu Leu Lys Asp Phe Cys Met Asn Pro Gln
Thr Val Leu Leu Arg Val Ile Ala Ala Phe Cys Phe Leu Gly Ile
                                      75
Leu Cys Ser Leu Ser Ala Phe Leu Leu Asp Val Phe Gly Pro Lys His
               85
Pro Ala Leu Lys Ile Thr Arg Arg Tyr Ala Phe Ala His Ile Leu Thr
                                                  110
                              105
Val Leu Gln Cys Ala Thr Val Ile Gly Phe Ser Tyr Trp Ala Ser Glu
                           120
                                              125
Leu Ile Leu Ala Gln Gln Gln His Lys Lys Tyr His Gly Ser Gln
                                          140
                       135
Val Tyr Val Thr Phe Ala Val Ser Phe Tyr Leu Val Ala Gly Ala Gly
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                   150
Gly Ala Ser Ile Leu Ala Thr Ala Ala Asn Leu Leu Arg His Tyr Pro
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Thr Glu Glu Glu Glu Gln Ala Leu Glu Leu Leu Ser Glu Met Glu Glu
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Asn Glu Pro Tyr Pro Ala Glu Tyr Glu Val Ile Asn Gln Phe Gln Pro
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Pro Pro Ala Tyr Thr Pro
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Gln Asn Val Val Pro Glu Ala Glu Gly Glu Asp Asp Pro Ala Gly Glu
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Ala Gln Ala Gly Arg Leu Pro Leu Pro Cys Ala Arg Ala Tyr Val
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Ser Pro Arg Ala Pro Phe Tyr Arg Pro Leu Ala Pro Glu Leu Arg Ala
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Arg Gln Leu Glu Leu Gly Ala Glu His Ala Leu Leu Leu Asp Ala Ala
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                                105
Gly Gln Val Phe Ser Trp Gly Gly Gly Arg His Gly Gln Leu Gly His
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Gly Thr Leu Glu Ala Glu Leu Glu Pro Arg Leu Leu Glu Ala Leu Gln
                        135
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Gly Leu Val Met Ala Glu Val Ala Ala Gly Gly Trp His Ser Val Cys
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Val Ser Glu Thr Gly Asp Ile Tyr Ile Trp Gly Trp Asn Glu Ser Gly
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Gln Leu Ala Leu Pro Thr Arg Asn Leu Ala Glu Asp Gly Glu Thr Val
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Ala Arg Glu Ala Thr Glu Leu Asn Glu Asp Gly Ser Gln Val Lys Arg
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Thr Gly Gly Ala Glu Asp Gly Ala Pro Ala Pro Phe Ile Ala Val Gln
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                                            220
Pro Phe Pro Ala Leu Leu Asp Leu Pro Met Gly Ser Asp Ala Val Lys
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                                        235
Ala Ser Cys Gly Ser Arg His Thr Ala Val Val Thr Arg Thr Gly Glu
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                                    250
                                                        255
Leu Tyr Thr Trp Gly Trp Gly Lys Tyr Gly Gln Leu Gly His Glu Asp
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                                                    270
                                265
Thr Thr Ser Leu Asp Arg Pro Arg Arg Val Glu Tyr Phe Val Asp Lys
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Gln Leu Gln Val Lys Ala Val Thr Cys Gly Pro Trp Asn Thr Tyr Val
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                                            300
Tyr Ala Val Glu Lys Gly Lys Ser
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eggttggage ageaaaagea geagataatg geagetttaa aeteceagae tgeegtgeag
ttccagcagt atgcagccca acagtatcca gggaactacg aacagcagca aattctcatc
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 <211> 97
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Arg Arg Ile Glu Glu Glu Arg Leu Arg Leu Glu Gln Gln Lys Gln Gln
                             40
Ile Met Ala Ala Leu Asn Ser Gln Thr Ala Val Gln Phe Gln Gln Tyr
Ala Ala Gln Gln Tyr Pro Gly Asn Tyr Glu Gln Gln Gln Ile Leu Ile
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                                         75
Arg Gln Leu Gln Glu Gln His Tyr Gln Gln Tyr Met Gln Gln Leu Tyr
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<212> PRT
<213> Homo sapiens
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<400> 6044

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gctgccactc aaacagagcc aggagaggag atgccagggc tgagtgtgag tgaggtggga

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1020
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Glu Val Ile Ala Val Val Met Asp Val Phe Thr Asp Ile Asp Ile Phe
Arg Asp Leu Gln Glu Ile Cys Arg Lys Gln Gly Val Ala Val Tyr Ile
                        55
Leu Leu Asp Gln Ala Leu Leu Ser Gln Phe Leu Asp Met Cys Met Asp
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70
Leu Lys Val His Pro Glu Gln Glu Lys Leu Met Thr Val Arg Thr Ile
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          85
Thr Gly Asn Ile Tyr Tyr Ala Arg Ser Gly Thr Lys Ile Ile Gly Lys
                      105 110
Val His Glu Lys Phe Thr Leu Ile Asp Gly Ile Arg Val Ala Thr Gly
                    120 125
Ser Tyr Ser Phe Thr Trp Thr Asp Gly Lys Leu Asn Ser Ser Asn Leu
  130 135
Val Ile Leu Ser Gly Gln Val Val Glu His Phe Asp Leu Glu Phe Arg
              150 155
Ile Leu Tyr Ala Gln Ser Lys Pro Ile Ser Pro Lys Leu Leu Ser His
           165 170 175
Phe Gln Ser Ser Asn Lys Phe Asp His Leu Thr Asn Arg Lys Pro Gln
       180 185 190
Ser Lys Glu Leu Thr Leu Gly Asn Leu Leu Arg Met Arg Leu Ala Arg
195 200 205
Leu Ser Ser Thr Pro Arg Lys Ala Asp Leu Asp Pro Glu Met Pro Ala
                215 220
Glu Gly Lys Ala Glu Arg Lys Pro His Asp Cys Glu Ser Ser Thr Val
              230 235 240
Ser Glu Glu Asp Tyr Phe Ser Ser His Arg Asp Glu Leu Gln Ser Arg
           245 250
Lys Ala Ile Asp Ala Ala Thr Gln Thr Glu Pro Gly Glu Glu Met Pro
      260 265 270
Gly Leu Ser Val Ser Glu Val Gly Thr Gln Thr Ser Ile Thr Thr Ala
     275 280 285
Cys Ala Gly Thr Gln Thr Ala Val Ile Thr Arg Ile Ala Ser Ser Gln
  290 295
                                300
Thr Thr Ile Trp Ser Arg Ser Thr Thr Thr Gln Thr Asp Met Asp Glu
    310 315 320
Asn Ile Leu Phe Pro Arg Gly Thr Gln Ser Thr Glu Gly Ser Pro Val
          325 330 335
Ser Lys Met Ser Val Ser Arg Ser Ser Ser Leu Lys Ser Ser Ser Ser
        340 345 350
Val Ser Ser Gln Gly Ser Val Ala Ser Ser Thr Gly Ser Pro Ala Ser
                    360 365
Ile Arg Thr Thr Asp Phe His Asn Pro Gly Tyr Pro Lys Tyr Leu Gly
                 375
Thr Pro His Leu Glu Leu Tyr Leu Ser Asp Ser Leu Arg Asn Leu Asn
              390
                             395
Lys Glu Arg Gln Phe His Phe Ala Gly Ile Arg Ser Arg Leu Asn His
                          410 415
           405
Met Leu Ala Met Leu Ser Arg Arg Thr Leu Phe Thr Glu Asn His Leu
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Gly Leu His Ser Gly Asn Phe Ser Arg Val Asn Leu Leu Ala Val Arg
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Asp Val Ala Leu Tyr Pro Ser Tyr Gln
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Arg Ser Cys Arg Pro Pro Gly Ser Ser Ser Gly Ser Pro Ser Ser Thr
                                25
Gly Thr Thr Leu Glu Lys Ser Cys Leu His His Cys Ser Gly Gly Gly
                            40
His Leu Pro Ser Ala Cys Leu Gly Ala Arg Arg Ser Ser Ser Leu Leu
                        55
Gly Tyr Gly Ser Cys Arg Asp Thr Gln Ser Trp Thr Pro Asp Pro Leu
                   70
Pro His Pro Pro Ser Leu Ser Pro Gln Ser Leu Leu Tyr Ser Gln Ala
                                    90
Met Arg Ser Pro Ile Ser His Gln Glu Leu Thr Arg Pro Leu Gly Lys
           100
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Glu Ala Ala Arg Arg Cys Gly His Thr Val Ala Leu Ser Ala Arg
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       115
                            120
Asp
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Ala Lys Lys Arg Lys Leu Asn Ser Ser Ser Ser Ser Ser Ser Asn Ser
                            40
Ser Asn Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Thr
Pro Pro Leu Gln Pro Arg Asp Ser Ala Ser Pro Ser Thr Ser Ser Phe
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                                        75
Cys Leu Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Gln Lys
                                    90
Lys Leu Arg Phe Glu Asp Thr Leu Glu Phe Val Gly Phe Asp Ala Lys
                                105
Met Ala Glu Glu Ser Ser Ser Ser Ser Ser Ser Ser Pro Thr Ala
                            120
                                                125
Ala Thr Ser Gln Glu Gln Gln Leu Lys Asn Lys Ser Ile Leu Ile Ser
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                                            140
Ser Val Gly Ser Val His His Ala Asp Gly Leu Ala Glu Ser Ser
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840		caatcaggca			
900	•	ggaccacata			
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catagatigg 1320	aaatggctat	tgcatttcac	tcaaatgctg	aaaagatttt	gcaggactgt
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	caagtgacat	ggcttctact	gcagaaaaca	tcagagacag	gatgaaacta
	aaaggcagca	gctgagacat	cctgaaatgg	tgaccacaga	gagctaatag

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1740
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Thr Gly His Glu Leu Leu Ser Glu Leu Gln Gln Arg Arg Phe Asn Gly
                            40
Ser Asp Gly Gly Val Ser Trp Ser Pro Met Asp Asp Glu Leu Leu Ala
                        55
Gln Pro Gln Val Met Lys Leu Leu Asp Ser Leu Arg Glu Gln Tyr Thr
Arg Tyr Gln Glu Val Cys Arg Gln Arg Ser Lys Arg Thr Gln Leu Glu
                                    90
Glu Ile Gln Gln Lys Val Met Gln Val Val Asn Trp Leu Glu Gly Pro
Gly Ser Glu Gln Leu Arg Ala Gln Trp Gly Ile Gly Asp Ser Ile Arg
                            120
Ala Ser Gln Ala Leu Gln Gln Lys His Glu Glu Ile Glu Ser Gln His
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135
Ser Glu Trp Phe Ala Val Tyr Val Glu Leu Asn Gln Gln Ile Ala Ala
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Leu Leu Asn Ala Gly Asp Glu Glu Asp Leu Val Glu Leu Lys Ser Leu
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Gln Gln Gln Leu Ser Asp Val Cys Tyr Arg Gln Ala Ser Gln Leu Glu
                              185
Phe Arg Gln Asn Leu Leu Gln Ala Ala Leu Glu Phe His Gly Val Ala
                          200
Gln Asp Leu Ser Gln Gln Leu Asp Gly Leu Leu Gly Met Leu Cys Val
                      215
                                         220
Asp Val Ala Pro Ala Asp Gly Ala Ser Ile Gln Gln Thr Leu Lys Leu
                   230
                                      235
Leu Glu Glu Lys Leu Lys Ser Val Asp Val Gly Leu Gln Gly Leu Arg
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Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
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Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
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Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
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Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
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Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
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Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
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Cys His Leu Thr Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala
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Thr Ala His Tyr Asp Pro Gly His Cys Phe Ala Glu Ser Arg Glu Leu
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Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile
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Ser Arg Ser Ser Glu Pro Pro Ala Cys Pro Arg His Trp Pro Cys Pro
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Pro Gly Leu Pro Phe Gly Gln Gly Ala Val Ala Arg Ala Ala Pro Cys
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Gly Val Pro Asn Val Gly Lys Ser Ser Leu Ile Asn Ser Leu Arg Arg
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Gln His Leu Arg Lys Gly Lys Ala Thr Arg Val Gly Gly Glu Pro Gly
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Arg Pro Ser Thr Leu Ser Arg Ala Leu Gln Ala Ser Gly Thr Cys Arg
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Pro Leu Cys Gly Phe Arg Leu Leu Thr Thr Leu Pro Ser Pro Pro Leu
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*** 1	T	nh -	T	325	¥	·	T	*	330	<b>~1</b>	T1.	7 w.w	*	335	***
vai	Leu	Pne	340	Arg	Leu	ıyr	Leu	345	GIN	GIY	116	AIG	350	ıyı	nis
C.~~	C114	y c.n		17-7	Glu	מות	Tire		Three	T.ou	) en	λνα		Val	Sar
SEL	GIY	355	ASP	VAL	GIU	Ala	360	GIU	ıyı	Deu	ASII	365	1113	Val	Jer
Ser	T.em		Ser	Tvr	Ile	Leu		His	Gln	Lvs	Trp		Ile	Cvs	Cvs
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AIG	Dea	ALG	500	1110	AL 9	GLy	7311	505	GAIL	عاد ت	ALU	711	510		Deu
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Signature   Sign															<b>(T)</b>	D
Name   Salu	Pro	Ser	Pro	Leu	Val	Thr	Met	Thr	Pro	Ala	Val	Pro	ATA	Val	Thr	Pro
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Secondary   Seco																
Secondary   Seco	Phe	Ser	Pro	Val	Arq	Arq	Phe	Ser	Asp	Gly	Ala	Ala	Ser	Ile	Gln	Ala
Part						_			_							
Second   S				** .		<b>~1</b>	T	Mot	C1		N cm	Car	Sar	TIA		Gln
Leu   Gln   Gln   Gln   Glu   Cys   Glu   Gln   Leu   Gln   Lys   Met   Tyr   Gly   Gly   Gln   Ile   S95   S95	Pne	Lys	Ala		Leu	GIU	гÀг	Mec		MSII	MSII	Ser	261		Lys	0.1.1
Asp         Glu         Arg         Thr         Leu         Glu         Lys         Thr         Gln         Gln         His         Ceu         Tyr         Gln           Gln         Glu         Arg         Thr         Leu         Glu         Fro         Gln         Gln         Gln         His         Jule         Gln													_			
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Asp         Glu         Arg         Thr         Leu         Glu         Lys         Thr         Gln         Gln         Gln         His         His         Gln         Gln         Gln         Gln         Gln         His         His         Gln         Gln <td></td> <td></td> <td></td> <td></td> <td>_</td> <td></td>					_											
Simple   S		<i>α</i> 3		Th~	LON	G1.,	Tare		Gln	Gln	Gln	His	Met	Leu	Tvr	Gln
Gln Glu Gln His His Gln IIe Leu Gln Gln Gln IIe Gln Asp Ser IIe  630  Cys Pro Pro Gln Pro Gs Pro Fro Gln Pro Ger Pro Gos Fro Gos Gos Gos Gos Gos Gos Gos Gos Gos Go	ASP		Arg	1111	neu	GIU			<b></b>	0					-3-	
630         Fro         Gln         Pro         Gln         Pro         Ser         Pro         Leu         Gln         Ala         Leu         Thr         Gln         Ala         Leu         Thr         His         Gln         Leu         Gln         Arg         Leu         Arg         Ile         Gln         Pro         Ser         Fro         Ser         Fro         Pro         Asn         Leu         Gln         Arg         Ile         Gln         Pro         Ser         Ser         Gln         Pro         Asn         Asn         Asn         His         Leu         Pro         Arg         Gln         Pro         Ser         Ser         Gln         Pro         Fro         Ser         Gln         Pro         Gln         Arg         Gln         Pro         Bro         Gln         Arg         Gln         Pro         Bro         Gln         Arg         Gln         Pro         Bro         Gln         Pro         Bro         Gln         Arg         Gln         Arg         Arg <td></td> <td>_</td> <td></td> <td></td>														_		
Cys         Pro         Pro         Gln         Pro         Ser         Pro         Leu         Gln         Ala         Ala         Cys         Glu         Asn         Gln         G55           Pro         Ala         Leu         Leu         Thr         His         Gln         Leu         Gln         Arg         Ile         Gln         Pro         Ser         G70         Ser         G70         Asn         Asn         Asn         Asn         His         Leu         Pro         Arg         Gln         Pro         Pro         Ser         G85         Asn         Asn         His         Leu         Pro         Hro         Arg         Gln         Pro         Hro         Arg         Gln         Pro         Hro         Arg         Arg         Ser         Arg	Gln	Glu	Gln	His	His	Gln	Ile	Leu	Gln	Gln	Gln	Ile	GIn	Asp	Ser	iie
Pro   Ala   Leu   Leu   Thr   His   Gln   Leu   Gln   Arg   Leu   Arg   Ile   Gln   Pro   Ser   665	630					635					640					
Pro   Ala   Leu   Leu   Thr   His   Gln   Leu   Gln   Arg   Leu   Arg   Ile   Gln   Pro   Ser   665	Cvs	Pro	Pro	Gln	Pro	Ser	Pro	Pro	Leu	Gln	Ala	Ala	Cys	Glu	Asn	Gln
Pro	Cys			<b></b>									-			
Ser         Pro         Pro         Pro         Asn         His         Pro         Asn         Asn         His         Leu         Pro         Arg         Gln         Pro         Ser         Ser         Ser         Ala         Met         Ile         Gln         Pro         His         Gly         Ala         Ala         Met         Ile         Gln         Pro         His         Gly         Ala         Ile         Gln         Pro         His         Gly         Ala         Ile         Fro         Arg         Ser         Ala         Ile         Fro         Arg         Ala         Ile         Pro         Ala         Ile         Pro         Ala         Ile         Pro         Arg         Ala         Ile         Pro         Pro         Pro         Ala         Ile         Pro         Pro         Pro         Ala <td></td> <td></td> <td></td> <td>_</td> <td></td> <td>•••</td> <td><b>01</b>-</td> <td>•</td> <td><b>01</b>-</td> <td></td> <td>T 011</td> <td>7 ~~</td> <td>T10</td> <td>Cl n</td> <td></td> <td>Sar</td>				_		•••	<b>01</b> -	•	<b>01</b> -		T 011	7 ~~	T10	Cl n		Sar
Ser         Pro         Pro         Pro         Asn         His         Pro         Asn         Asn         Leu         Phe         Arg         Gln         Pro         Ser           Asn         Ser         Pro         Pro         Pro         Met         Ser         Ser         Ala         Met         Ile         Gln         Pro         His         Gly         Ala         Met         Gln         Pro         695	Pro	Ala	Leu		Thr	HIŞ	GIR	Leu		Arg	Leu	ALG	TIE		PIO	361
Asn Ser Pro Pro Pro Pro Pro Ser Ser Ser Ala Met I le Gln Pro His Gly Ala 690																
Asn Ser Pro Pro Pro Pro Pro Ser Ser Ser Ala Met I le Gln Pro His Gly Ala 690	Ser	Pro	Pro	Pro	Asn	His	Pro	Asn	Asn	His	Leu	Phe	Arg	Gln	Pro	Ser
Asn         Ser         Pro         Pro         Pro         Met         Ser         Ser         Ala         Met         Title         Gln         Gln         Fro         Fro         Fro         His         Gly         Ala         Fro         Fro         Fro         Ala         Ile         Pro         Ala         Ile         Pro         Pro </td <td></td>																
Ala Ser Ser Ser Gln Phe Gln Gly Leu Pro Ser Arg Ser Ala Ile Phe 705	200	Sar		Pro	Pro	Met	Ser	Ser	Ala	Met	Ile	Gln	Pro	His	Glv	Ala
Ala         Ser         Ser         Gen         Phe         Gln         Gly         Leu         Pro         Ser         Arg         Ser         Ala         Ile         Phe           705	ASII		FIO	110	110											
705								_,					C	77-	T1.	Dho
Gln Gln Gln Pro Glu Asn Cys Ser Ser Pro Pro Asn Val Ala Leu Thr 725  Cys Leu Gly Met Gln Gln Pro Ala Gln Ser Gln Gln Val Thr Ile Gln 740  Val Gln Glu Pro Val Asp Met Leu Ser Asn Met Pro Gly Thr Ala Ala 755  Gly Ser Ser Gly Arg Gly Ile Ser Ile Ser Pro Ser Ala Gly Gln Met 770  Gln Met Gln His Arg Thr Asn Leu Met Ala Thr Leu Ser Tyr Gly His 785  Arg Pro Leu Ser Lys Gln Leu Ser Ala Asp Ser Ala Glu Ala His Ser 805  Leu Asn Val Asn Arg Phe Ser Pro Ala Asn Tyr Asp Gln Ala His Leu 820  His Pro His Leu Phe Ser Asp Gln Ser Arg Gly Ser Pro Ser Ser Tyr 835  Ser Pro Ser Thr Gly Val Gly Phe Ser Pro Thr Gln Ala Leu Lys Val 850  Pro Pro Leu Asp Gln Phe Pro Thr Phe Pro Pro Ser Ala His Gln Gln 865  Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro 886	Ala	Ser	Ser	Ser	Gln	Phe	GIn	GIA	Leu	Pro		Arg	Ser	Ala	TIE	
Cys Leu Gly Met Gln Gln Pro Ala Gln Ser Gln Gln Val Thr Ile Gln 740	705															
Cys Leu Gly Met Gln Gln Pro Ala Gln Ser Gln Gln Val Thr Ile Gln 740	Gln	Gln	Gln	Pro	Glu	Asn	Cys	Ser	Ser	Pro	Pro	Asn	Val	Ala	Leu	Thr
Cys         Leu         Gly         Met         Gln         Gln         Pro         Ala         Gln         Ser         Gln         Gln         Thr         Ile         Gln           Val         Gln         Glu         Pro         Val         Asp         Met         Leu         Ser         Asn         Met         Pro         Gly         Thr         Ala			-				_									
Val       Gln       Gln       Gln       Pro       Val       Asp       Met       Leu       Ser       Asn       Met       Pro       Gly       Thr       Ala       Ala         Gly       Ser       Ser       Gly       Arg       Gly       Ile       Ser       Ile       Ser       Pro       Ser       Ala       Gly       Gln       Met         Gln       Met       Gln       His       Arg       Thr       Asn       Leu       Met       Ala       Thr       Leu       Ser       Tyr       Gly       His         Arg       Pro       Leu       Ser       Lys       Gln       Leu       Ser       Ala       Asp       Ser       Ala       Ala       Glu       Ala       Glu       Ala       Glu       Ala       Glu       Ala       Glu       Ala       Glu       Ala       Ala       Ala       Asp       Glu       Ala       A	<b>a</b>		<b>61.</b>	M-+		C1 n	Dro	715	Gl n		Gln	Gln	Val	Thr	Tle	Gln
Val         Glu         Pro         Val         Asp         Met         Leu         Ser         Asn         Met         Pro         Gly         Thr         Ala         Ala           Gly         Ser         Ser         Gly         Arg         Gly         Ile         Ser         Ile         Ser         Pro         Ser         Ala         Gly         Gln         Met           Gln         Met         Gln         His         Arg         Thr         Asn         Leu         Met         Ala         Thr         Leu         Ser         Ala         Ser         Tyr         Gly         His         Ala         Ala         Thr         Leu         Ser         Ala         Ala         Ala         Thr         Leu         Ser         Ala         Ala         Asp         Ser         Ala         His         Ala         Ala         Asp         Ser         Ala         Ala         Asp         Ser         Ala         Ala         Asp         Ala         Ala         Asp         Gln         Ala         Ala         Asp         Gln         Ala         Ala         Asp         Gln         Ala         Ala         Ala         Ala         Ala         Ala	Cys	Leu	GIY		GIII	GIII	FIO	AIG		501	<b>0111</b>	<b></b>				
Ser   Ser   Ser   Gly   Arg   Gly   Ile   Ser   Ile   Ser   Pro   Ser   Ala   Gly   Gln   Met   Arg   Gly   Ile   Ser   Ile   Ser   Pro   Ser   Ala   Gly   Gln   Met   Arg   Fro   Fro												_				
Gly Ser Ser Gly Arg Gly Ile Ser Ile Ser Pro Ser Ala Gly Gln Met 770	Val	${\tt Gln}$	Glu	Pro	Val	Asp	Met	Leu	Ser	Asn	Met	Pro	GIA	Thr	Ala	Ala
Ser   Ser			755					760					765			
Ser   Ser	Glv	Ser	Ser	Glv	Ara	Glv	Ile	Ser	Ile	Ser	Pro	Ser	Ala	Gly	Gln	Met
Gln Met Gln His Arg Thr Asn Leu Met Ala Thr Leu Ser Tyr Gly His 785	UL,			<b>U</b> -1	5									-		
785       790       795       795       800         Arg       Pro       Leu       Ser       Lys       Gln       Leu       Ser       Ala       Asp       Ser       Ala       Glu       Ala       Ala       Asp       Ser       Ala       Asp       Asp       Gln       Asp       Tyr       Asp       Ala       Asp       Fro       Ala       Asp       Gln       Asp       Ala       Asp       Asp       Gln       Asp       A					-	m\	-	T	Man	27-	The		C0*	T3 12	Clir	uic
Arg Pro Leu Ser Lys Gln Leu Ser Ala Asp Ser Ala Glu Ala His Ser 810	Gln	Met	GIn	His	Arg	Thr	ASII	Leu	Met			Leu	361	TYL	GIY	
Leu Asn Val Asn Arg Phe Ser Pro Ala Asn Tyr Asp Gln Ala His Leu 820       825       825       830       830       830       830       830       830       840       825       840       830       830       840       830       840       830       840       845       845       840       845											-					
Leu Asn Val Asn Arg Phe Ser Pro Ala Asn Tyr Asp Gln Ala His Leu 820       825       825       830       830       830       830       830       830       840       825       840       830       830       840       830       840       830       840       845       845       840       845	Arq	Pro	Leu	Ser	Lys	Gln	Leu	Ser	Ala	Asp	Ser	Ala	Glu	Ala	His	Ser
Leu Asn Val Asn Arg Phe Ser Pro Ala Asn Tyr Asp Gln Ala His Leu 820																
His       Pro       His       Leu       Phe       Ser       Asp       Gln       Ser       Arg       Gly       Ser       Pro       Ser       Tyr         Ser       Pro       Ser       Thr       Gly       Val       Gly       Phe       Ser       Pro       Thr       Gln       Ala       Leu       Lys       Val         Pro       Pro       Leu       Asp       Gln       Phe       Pro       Pro       Pro       Pro       Pro       Pro       Pro       Pro       Ser       Ala       His       Gln       Gln       Gln       Ala       Leu       Ser       Pro         Pro       Pro       His       Tyr       Thr       Thr       Ser       Ala       Leu       Gln       Gln       Ala       Leu       Ser       Pro         Pro       Pro       His       Tyr       Thr       Thr       Ser       Ala       Leu       Gln       Gln       Ala       Leu       Ser       Pro         Pro       Pro       His       Ser       Thr       Thr       Ser       Ala       Leu       Gln       Gln       Ala       Leu       Leu       Ser       Pro       P	T	N	17-1	7 ~~		Pho	Co~	Pro	λla		TVY	Σen	Gln	Ala	His	Leu
His Pro His Leu Phe Ser Asp Gln Ser Arg Gly Ser Pro Ser Ser Tyr 835	Leu	ASII	val		ALG	FILE	Ser	FIU		ng.	-1-	rop				
Ser       Pro       Ser       Thx       Gly       Val       Gly       Phe       Ser       Pro       Thx       Gln       Ala       Leu       Lys       Val         Pro       Pro       Pro       Leu       Asp       Gln       Phe       Pro       Phe       Pro       Pro       Pro       Ser       Ala       His       Gln       G															_	_
Ser       Pro       Ser       Thx       Gly       Val       Gly       Phe       Ser       Pro       Thx       Gln       Ala       Leu       Lys       Val         Pro       Pro       Pro       Leu       Asp       Gln       Phe       Pro       Phe       Pro       Pro       Pro       Ser       Ala       His       Gln       G	His	Pro	His	Leu	Phe	Ser	Asp	Gln	Ser	Arg	Gly	Ser	Pro	Ser	Ser	Tyr
Ser       Pro       Ser       Thr       Gly       Val       Gly       Phe       Ser       Pro       Thr       Gln       Ala       Leu       Lys       Val         850       850       860       8																
Pro       Pro       Leu Asp       Gln       Phe       Pro       Thr       Phe       Pro       Pro       Pro       Ser       Ala His       Gln       Gln       Gln       Gln       Fro       Pro       His       Tyr       Thr       Thr       Ser       Ala       Leu       Gln       Gln       Ala       Leu       Leu       Ser       Pro       Pro       His       New       New       Pro       New	6~~	D~~		Thr	G1 v	۷a۱	Glv	-	Ser	Pro	Thr	Gln	Ala	Leu	Lvs	Val
Pro Pro Leu Asp Gln Phe Pro Thr Phe Pro Pro Ser Ala His Gln Gln 865 870 875 885  Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro 885 890 895	361		JEL	* ***	GLY	141									-2-	
865 870 875 880 Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro 885 890 895						_				_	_					<b>~</b> 3
Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro 885 890 895	Pro	Pro	Leu	Asp	Gln	Phe	Pro	Thr	Phe	Pro	Pro	Ser	Ala	HlS	GIN	
Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro 885 890 895												•				
885 890 895		Pro	His	Tvr	Thr	Thr	Ser	Ala	Leu	Gln	Gln	Ala	Leu	Leu	Ser	Pro
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Thr Pro Pro Asp Tyr Thr Arg His Gin Gin vai Pro His 11e Leu Gin		_	_	_		m1	3	112 -	<b>61</b> -		17m 7	Dros	ui-	Tla		G1 ~
	Thr	Pro	PLO	Asp	Tyr	Inr	Arg	uts	GIII	GTI	val	PIO	UTS	116	ساجلا	3211

900

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                    950
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 Gly Gly Gln Ser Met Thr Glu Arg Gln Ala Leu Ser Tyr Gln Asn Ala
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 Asp Ser Tyr His His Thr Ile Gln Asn Ser Asp Asp Ala Tyr Val Gln
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                                  1050
Gly Gly His Glu His Pro Asp Leu Ser Asp Gly Ser Gln His Leu Asn
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                                                 1070
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Ile His Leu Gly Pro Arg Gln Ala Val Arg Pro Ser Val Arg Ala Glu
Ser Arg Arg Val Asp Gly Gly Gly Arg Ser Pro Arg Glu Pro Asp Gly
Arg Gly Arg Ser Arg Gln Ala Arg Phe Ser Pro Tyr Pro Ile Pro Ala
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	Δla	21 s	Ala	_	Gly	Dro	Gl.	Dro		Mor	Dwa	Dwa	2 ~~		Mot
ALG	AT G	A.a	20	GIII	GIY	PIO	GIU	25	GIY	Met	PIO	Pro	30	PIO	Mec
Δen	Ser	Thr	Gln	Pro	Car	The	בות		Mat	Tura	T	C		D×o	Dho
A311	361	35	GIII	PIU	Set	1111	40	GIY	MEL	гàг	пр	-	Leu	PIO	Pile
Hic	T.011		Cys	λνα	Clv	Dro		C1.	· co-	T 011	C	45	Drea	Dwa	27-
1113	50	Deu	Cys	Arg	Gry	55	261	GIY	Ser	Leu	60	Ala	PLO	PIO	Ald
Δla		Va 1	Ile	Ser	A1=		Pro	50~	car	5a~		λ <b>~~</b> ~	ui c	71 ~~~	Tare
65				-	70	110	-10	561	561	75	361	AT 9	1113	n.a	80
	Arg	Ara	Thr	Ser		Lvs	Ser	Glu	Δla		λla	Ara	Glv	Glv	
	5			85		-1-			90	<b>-</b> -,		••••	<b>U</b> -1	95	0-7
Gln	Gly	Ser	Lys		Lvs	Glv	Ara	Glv		Tro	G1v	Glv	Ara		His
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His	His	His	Pro	Leu	Pro	Ala	Ala	Gly	Phe	Lvs	Lvs	Gln		Arq	Lvs
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Phe	Gln	Tyr	Gly	Asn	Tyr	Cys	Lys	Tyr	Tyr	Gly	Tyr	Arq	Asn	Pro	Ser
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Arg	Asp	Val	Leu	Asp	Leu	Gly	Cys	Asn	Val	Gly	His	Leu	Thr	Leu	Ser
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Ile	Ala	Cys	Lys	Trp	Gly	Pro	Ser	Arg	Met	Val	Gly	Leu	Asp	Ile	Asp
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Ser	Arg		Ile	His	Ser	Ala		Gln	Asn	Ile	Arg	His	Tyr	Leu	Ser
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GIu		Leu	Arg	Leu	Pro		Gln	Thr	Leu	Glu		Asp	Pro	Gly	Ala
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	car	Lau	Thr	ת ה		λ ~~~	C1	Dwa	T1.0	235	71.	D==	C1 -	37-7	240
ATG	261	neu	1111	245	Ser	Arg	GIY	PLO	250	ALG	ALA	PIO	GIII	255	PIO
T.ess	Asp	Glv	Ala		Thr	Ser	Va 3	Dhe		Acn	Aen	V-1	Va 1		1/a 1
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		275	-2-				280	р				285			• • • • • • • • • • • • • • • • • • • •
Pro	Glu	Tyr	Asp	Val	Val	Leu	Cys	Leu	Ser	Leu	Thr		Trp	Val	His
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Arg	His	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Val	Leu	Glu	Pro	Gln	Pro	Trp
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Ser	Ser	Tyr	Gly	Lys	Arg	Lys	Thr	Leu	Thr	Glu	Thr	Ile	Tyr	Lys	Asn
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Tyr	Tyr	Arg	Ile	Gln	Leu	Lys	Pro	Glu	Gln	Phe	Ser	Ser	Tyr	Leu	Thr
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Ser		Asp	Val	Gly	Phe		Ser	Tyr	Glu	Leu	Val	Ala	Thr	Pro	His
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Pro Ala Cys Leu Leu Gly Arg Pro Trp Met Ser Arg Arg Cys Ser Arg
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Leu Gly Ser Thr Pro Pro Pro Ala Pro Ala Ser Pro Val Glu Ser Pro
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Arg Pro Ser Pro Ala Ser Ser Ala Phe Ser Ser Leu Pro Ser Asp Gly
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Trp Gly Ser Ser Val Gly Ser Gly Leu Pro Trp Pro Ala Thr Arg Trp
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Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg
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Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu
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                                       75
Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp
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Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
                               105
Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
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Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala
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Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu
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                           200
Leu Cys Leu Ala Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu
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Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly
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Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln Ser
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Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu
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 Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys
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Pro Leu Pro Gly Phe Lys Gln Phe Ser Cys Arg Ser Leu Pro Ser Ser
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                            40
Trp Asp Tyr Arg His Ala Pro Pro Arg Gln Ala Asn Phe Cys Ile Phe
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                        55
                                            60
Ser Arg Asp Gly Val Ser Pro Cys Trp Pro Gly Trp Ser Gln Thr Pro
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Asp Leu Arg Arg Ser Thr His Leu Ser Val Pro Lys Cys Trp Asp Tyr
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Arg Arg Glu Pro Pro His Leu Ala Tyr Glu Trp Ser Phe Asn
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Pro Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Glu Glu
Ala Glu Leu Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys
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Leu Asp Arg Gln Lys Glu Leu
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Pro Gln Phe Pro Gln Arg Asn Arg Leu Leu Ala Ser Arg Val Gly Tyr
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Arg Val Ser Val Leu His Gly Ile Tyr Glu Asp Val Pro Pro Lys Leu
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                                        75
Leu Pro Pro Pro Pro Trp Asp Ala Thr Val Arg Pro Ala Asp Glu Phe
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Leu Pro Gln Arg Pro Arg Glu Gly Gly Leu Arg Ala Ala Ala Ala Ala
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Thr Gly Gly Glu Ala Ser Ala Gly Asn Leu Gly Pro Gly Gly Ala Arg
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25

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Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
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Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
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Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
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Lys Cys Phe Asn Pro Thr Ser Pro Leu Ser Leu Pro Leu Ser Cys Pro
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Tyr Pro Leu Val Glu His Val Cys Pro Lys Arg Pro Cys Lys Val Cys
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Cys Pro Val Leu Ser Gly Leu Cys Gln Gly Ile Lys Leu Leu Leu
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FIO	Mec	ייי	Val	245	110		-		250		-,-			255	
D=0	7~~	T ***	G1v		Lvc	Mot	ጥኒኒን	Glv	Leu	LVC	Ser	Tvr	Tle		Tvr
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Asp	Phe	35	Ald	. val	Arg	val	40	AIG	ALA	vaı	Ата		Inr	Ala	. val
Tla	C ~~		λοπ	The same		The		Tan	7			45	TT0 ***	<b>~1.</b>	Ser
116	50	ıyı	ASP	ıyı	Leu	55	Ser	ьец		Ser	60	PIO	Tyr	GIY	Set
C1.,		Tries	Tan	C1 n	Ton		Car	Tre	T] 0	Wie		T 011	Dho	~1 <u>-</u>	Ser
65	GIU	TAT	Leu	GIII	70	Arg	361	БÃЗ	116	75	Asp	reu	Pne	GIII	80
	3	*	mb			~1	mb		C	_		<b>~</b> 1	*** 7	***	Lys
Pne	ASp	ASP	1111	85	Deu	GIY	IIIL	Ala	90	Leu	AId	GIII	vai		гÀг
	**- 7	<b>T</b>	TT-1 _		<b>~1</b>	N	(T)	*** 7		**- 7	*	**- 1	<b>~</b> 3	95	D
Ala	vai	Leu		_	GIY	Arg	III			Val	ьys	vai		HIS	Pro
T	11-1	7	100		C 0 30	C	7	105		T	T	Man	110	17.a. T	T
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val	130	ALA	vaı	nys	GIII	135		PIO	GIU	Pile	140	Pile	Met	пр	Deu
Wa I		C1	777	Tura	Taro			Dro	T 011	C1.,		7	Dho	T 011	7 ~~
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	G11/	7 ~~	) CD	אן א	Glu	Tara	V-1	C-~	Cl n			7 ~~	uia	Dho	_
Giu	GIY	ALG	ASII	165	GIU	пуs	·val	SEL	170		neu	Arg	nis	175	_
Dho	T 011	Tara	W-1		7 ~~~	Tlo	u: -	m			C 0 ==	mb	<b>~</b> 1		
Pne	теп	nys	180		Arg	TIE	nis	185	ASP	Leu	Ser	IIII	190	Arg	Val
T ou	T 011	Mat			นาไ	7.00	C1		C1 n	17-1	7	7 ~~		N cm	Tyr
Deu	Deu	195	GIU	FILE	val	ASP	200	Gly	GIII	var	ASII	205	Arg	ASP	IÀI
Mot	C1		N an	Tura	T10	7		<b>N</b> ==	<b>~1.</b> ,	Tlo	C		1115.0	T 011	C1
Mec	210	ALG	ASII	гÃР	Ile	215	vaı	ASII	GIU	116	220	Arg	nis	Leu	GIY
Tue		There	C0*	GI.	Met		Dhio	17-1	Non.	G) v		17-1	Wis	Cree	) an
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	Wie	Pro	G) v	) cn	Val	LAN	1751	7 ~~	Lave		Pro	Gly	Thr	Gly	
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A.J.	290	_,_	9	• • • •	_, _	295	-1-	501	0111		300			01,	p
T.em		Pro	Len	Phe	Ala		Met	T.en	Thr	Δla		Ser	Trm	Asp	Ser
305	-7-				310	-,-				315	5				320
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Pro Gln Glu Glu Arg Glu Thr Gln Val Ala Ala Trp Leu Lys Lys Ile
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Phe Gly Asp His Pro Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr
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Glu Ile Leu His His Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Asp
Val Tyr Leu Val Ile Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu
Ser Glu Ala Lys Tyr Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe
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Ser Pro Ala Asn Leu Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu
                               105
Val Asp Ser Ala Val Ala Leu Glu Thr Lys Asp Thr Ser Leu Ala Ser
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Phe Ile Pro Ala Val Asn Asp Leu Thr Ser Asp Leu Phe Arg Thr Lys
                       135
Ser Lys Ser Glu Glu Ile Lys Ile Glu Leu Glu Lys Leu Glu Lys Asn
                                      155
                   150
Leu Thr Ala Thr Leu Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys
                                   170
               165
Lys Ala Glu Leu His Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg
                               185 ·
Arg Gln Asn Met Asp Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe
                           200
Gly Ile Lys Ala Ala Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala
                                          220
                       215
Ser Leu Ser His Gln Ser Leu Val Ala Leu Ser Glu Lys Leu Ala Arg
                   230
                                      235
Leu Lys Gln Gln Thr Ile Pro Leu Lys Lys Lys Leu Glu Ser Tyr Leu
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Asp Leu Met Pro Asn Pro Ser Leu Ala Gln Val Lys Ile Glu Glu Ala
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Lys Arg Glu Leu Asp Ser Ile Glu Ala Glu Leu Thr Arg Arg Val Asp
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caaggeetgt tgatgeagee atgggegtgg ctacagettg cagagaacte cetettggee
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gatggaaagc cctttgtcat gaatctgcag gatctgtata tggcagtcac cacacaagag
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aagttgatgt tgacaggccc acagggaatt ggccttccct gttcaagtgg aagccagtct
ctgagaatcc cgtgctctcc tctcttttgg tggaggttct gtaggttcag gtttctacca
tggactttag gtatataggg caagtcagca agaaagcacc acacactcag gaagccttgt
1320
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1483
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Gly Tyr Ala Leu Leu Val Ser Asp Leu Gln Gln Val Trp His Glu Gln
                           40
Val Asp Thr Ser Val Val Ser Gln Arg Ala Lys Glu Leu Asn Lys Arg
Leu Thr Ala Pro Pro Ala Ala Phe Leu Cys His Leu Asp Asn Leu Leu
                    70
Arg Pro Leu Leu Lys Asp Ala Ala His Pro Ser Glu Ala Thr Phe Ser
                85
                                   90
Cys Asp Cys Val Ala Asp Ala Leu Ile Leu Arg Val Arg Ser Glu Leu
                               105
Ser Gly Leu Pro Phe Tyr Trp Asn Phe His Cys Met Leu Ala Ser Pro
                           120
Ser Leu Val Ser Gln His Leu Ile Arg Pro Leu Met Gly Met Ser Leu
                        135
                                           140
Ala Leu Gln Cys Gln Val Arg Glu Leu Ala Thr Leu Leu His Met Lys
                   150
                                        155
Asp Leu Glu Ile Gln Asp Tyr Gln Glu Ser Gly Ala Thr Leu Ile Arg
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                                   170
Asp Arg Leu Lys Thr Glu Pro Phe Glu Glu Asn Ser Phe Leu Glu Gln
                               185
Phe Met Ile Glu Lys Leu Pro Glu Ala Cys Ser Ile Gly Asp Gly Lys
                           200 .
                                               205
Pro Phe Val Met Asn Leu Gln Asp Leu Tyr Met Ala Val Thr Thr Gln
                       215
                                           220
Glu Val Gln Val Gly Gln Lys His Gln Gly Ala Gly Asp Pro His Thr
                   230
                                       235
Ser Asn Ser Ala Ser Leu Gln Gly Ile Asp Ser Gln Cys Val Asn Gln
                                   250
                245
Pro Glu Gln Leu Val Ser Ser Ala Pro Thr Leu Ser Ala Pro Glu Lys
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Glu Ser Thr Gly Thr Ser Gly Pro Leu Gln Arg Pro Gln Leu Ser Lys
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Val Lys Arg Lys Asn Pro Arg Gly Leu Phe Ser
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120
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aaaactgttc agtttggtgg aactgtgaca gaagtcttgc tgaagtacaa aaagggtgaa
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Gly Glu Thr Asn Asp Phe Glu Leu Leu Lys Asn Gln Leu Leu Asp Pro
                             40
Asp Ile Lys Arg Leu Pro Trp Leu Asn Arg Ser Gln Thr Val Val Glu
Glu Tyr Leu Ala Phe Leu Gly Asn Leu Val Ser Ala Gln Thr Val Phe
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Leu Arg Pro Cys Leu Ser Met Ile Ala Ser
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tccctgagtg tggaagagca gctgtcactc atcagtggtt gtcccaatat ccaagaagca
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tgtctcatgc cttccaagtt gtttgctggc ttggtccatg tgaagcaatg catcgtggct
540
catectgtga atecgecata ctacateceg etggttgage tggteececa eceggagaeg
 600
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gecectaega cagtggaeag aacceaegee etgatgaaga agattggane agtgeeceat
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gagtgcctca tgagactcgc caagttgaag agtcaagtgc agccccagtg aatttcttgt
aatgcagett ceaeteetet cattggagge eetatttggg aacaetgcaa geeettaate
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Ser Gly Gly Phe Gln Val Lys Leu Tyr Asp Ile Glu Gln Gln Ile
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                                25
Arg Asn Ala Leu Glu Asn Ile Arg Lys Glu Met Lys Leu Leu Glu Gln
Ala Gly Ser Leu Lys Gly Ser Leu Ser Val Glu Glu Gln Leu Ser Leu
                        55
Ile Ser Gly Cys Pro Asn Ile Gln Glu Ala Val Glu Gly Ala Met His
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Ile Gln Glu Cys Val Pro Glu Asp Leu Glu Leu Lys Lys Ile Phe
Ala Gln Leu Asp Ser Ile Ile Asp Asp Arg Val Ile Leu Ser Ser
                                105
            100
Thr Ser Cys Leu Met Pro Ser Lys Leu Phe Ala Gly Leu Val His Val
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120
Lys Gln Cys Ile Val Ala His Pro Val Asn Pro Pro Tyr Tyr Ile Pro
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Leu Val Glu Leu Val Pro His Pro Glu Thr Ala Pro Thr Thr Val Asp
                                        155
                    150
Arg Thr His Ala Leu Met Lys Lys Ile Gly Xaa Val Pro His Ala Ser
                                    170
Pro Glu Gly Gly Arg Leu Arg Ser Glu Pro Pro Ala Ile Cys Asn
            180
His Gln Arg Gly Leu Ala Ala Ser Gly Gly Arg Asn Xaa Cys Leu Leu
                            200
Val Thr Trp Xaa Leu Val Met Ser Glu Gly Leu Gly Met Arg Tyr Ala
                                            220
                        215
Phe Ile Gly Pro Leu Glu Thr Met His Leu Asn Ala Glu Gly Met Leu
225
Ser Tyr Cys Asp Arg Tyr Ser Glu Gly Ile Lys His Val Leu Gln Thr
                245
Phe Gly Pro Ile Pro Glu Phe Ser Arg Ala Thr Ala Glu Lys Val Asn
                                265
            260
Gln Asp Met Cys Met Lys Val Pro Asp Asp Pro Glu His Leu Ala Ala
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Ser Gln Val Gln Pro Gln
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660
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actttgaatc 960	cttttcttcg	ggcctgtgct	gagttacacc	agaatgtaaa	tgtgaagaac
ataatcattg 1020	ctttaattga	tagattagct	ttatttgctc	accgtgaaga	tggacctgga
1080		ttttgatata			
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gccatgaaat 1200	gttaccctga	tcgtgtggac	tatgttgata	aagttctaga	aacaacagtg
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ttaaaacatt 1380	ttcacccact	ctttgagtac	tttgactacg	agtccagaaa	gagcatgagt
tgttatgtgc 1440	ttagtaatgt	tctggattat	aacacagaaa	ttgtctctca	agaccaggtg
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tctggcagaa 2160	acacggacaa	aaatggggag	gagcttcacg	gaggcaagag	ggtaatggag
tgcctaaaaa 2220	aagctctaaa	aatagcaaat	cagtgcatgg	acccctctct	acaagtgcag
ctttttatag 2280	aaattctgaa	cagatatatc	tatttttatg	aaaaggaaaa	tgatgcggta
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acaattcagg ttttaaacca gcttatccaa aagattcgag aagacctccc gaatcttgaa
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Asp Leu Tyr Glu Leu Val Gln Tyr Ala Gly Asn Ile Ile Pro Arg Leu
                        55
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Tyr Leu Leu Ile Thr Val Gly Val Val Tyr Val Lys Ser Phe Pro Gln
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Ser Arg Lys Asp Ile Leu Lys Asp Leu Val Glu Met Cys Arg Gly Val
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Gln His Pro Leu Arg Gly Leu Phe Leu Arg Asn Tyr Leu Leu Gln Cys
                                                    110
                                105
Thr Arg Asn Ile Leu Pro Asp Glu Gly Glu Pro Thr Asp Glu Glu Thr
Thr Gly Asp Ile Ser Asp Ser Met Asp Phe Val Leu Leu Asn Phe Ala
                        135
                                            140
Glu Met Asn Lys Leu Trp Val Arg Met Gln His Gln Gly His Ser Arg
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                                        155
Asp Arg Glu Lys Arg Glu Arg Glu Arg Gln Glu Leu Arg Ile Leu Val
                                    170
Gly Thr Asn Leu Val Arg Leu Ser Xaa Ser Trp Arg Cys Lys Cys Gly
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Thr Leu Gln Gln Ile Val Leu Thr Gly Ile Leu Glu Gln Val Val Asn
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Cys	Arq			Leu	Ala	Gln		Tyr	Leu	Met	Glu		Ile	Ile	Gln
- 4 -	210	•				215		_			220	-			
Val	Phe	Pro	Asp	Glu	Phe	His	Leu	Gln	Thr	Leu	Asn	Pro	Phe	Leu	Arg
225					230				•	235					240
Ala	Cys	Ala	Glu	Leu	His	Gln	Asn	Val	Asn	Val	Lys	Asn	Ile	Ile	Ile
				245					250					255	
Ala	Leu	Ile	Asp	Arg	Leu	Ala	Leu	Phe	Ala	His	Arg	Glu	Asp	Gly	Pro
			260					265					270		
Gly	Ile	Pro	Ala	Asp	Ile	Lys		Phe	Asp	Ile	Phe		Gln	Gln	Val
		275					280				_	285			
Ala		Val	Ile	Gln	Ser		Gln	Asp	Met	Pro		GIU	Asp	vai	Val
	290			_		295		•		<b>M</b>	300	<b>C</b>	Ma can	D	7
	Leu	Gln	Val	ser		ire	ASD	Leu	Ala		ьys	Cys	Tyr	PIO	Asp 320
305	**- 3			17- 3	310	T	17-3	7 011	C1	315 Thr	Thr	17-1	GI.	Tla	
Arg	vaı	Asp	Tyr		Asp	гуг	vaı	neu	330	IIII	1111	Val	GIU	335	FIIC
7 ~~	T 1.0	T 011	) co	325	Gli	wie	Tla	212		Ser	Ser	Δla	Val		Lys
ASII	ьуs	Leu	340	Leu	GIU	nis	116	345	1111	Jer	561	AIG	350	561	و رك
Glu	T.011	Thr		T.e.11	T.e.u	T.vs	Tle		Val	Asp	Thr	Tvr		Asn	Ile
GIU	пец	355	~~3	204	200	-,-	360					365			
T.eu	Thr		Leu	Lvs	Leu	Lvs		Phe	His	Pro	Leu		Glu	Tyr	Phe
204	370			-1-		375					380			•	
Asp		Glu	Ser	Arq	Lys		Met	Ser	Cys	Tyr	Val	Leu	Ser	Asn	Val
385	- 2 -			_	390				-	395					400
Leu	Asp	Tyr	Asn	Thr	Glu	Ile	Val	Ser	Gln	Asp	Gln	Val	Asp	Ser	Ile
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Met	Asn	Leu	Val	Ser	Thr	Leu	Ile	Gln	Asp	Gln	Pro	Asp	Gln	Pro	Val
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Glu	Asp	Pro	Asp	Pro	Glu	Asp		Ala	Asp	Glu	Gln		Leu	Val	Gly
		435					440	_				445		_	
Arg		Ile	His	Leu	Leu		Ser	Glu	Asp	Pro		Gln	Gin	Tyr	Leu
	450		_,			455		<b>51</b> -	<b>~</b> 3		460	<b>63</b>	3	<b>61</b> -	N
	Leu	Asn	Thr	Ala		rys	HIS	Pne	GIĄ	475	GIA	GIY	ASII	GIII	Arg 480
465	<b>3</b>	Dh.a	mh	T 011	470 Dro	D~0	T 033	v.	Dhe	Ala	71=	Tur	Gl n	T.e.11	
TTE	Arg	Pne	THE	485	PIO	PIO	Leu	vai	490	AIG	ALG	LYL	<b>G111</b>	495	n.u.
Dhe	λνα	ጥረታ	Lve		Δen	Ser	T.vs	Tro		Thr	Asn	Glv	Lvs		Asn
FIIC	AL 9	- 7 -	500	014		501	_,_	505				,	510	5	
Ala	Arg	Arg		Phe	His	Leu	Pro		Gln	Thr	Ile	Ser	Ala	Leu	Ile
		515										525			
Lys	Ala	Glu	Leu	Ala	Glu	Leu	Pro	Leu	Arg	Leu	Phe	Leu	Gln	Gly	Ala
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Leu	Ala	Ala	Gly	Glu	Ile	Gly	Phe	Glu	Asn	His	Glu	Thr	Val	Ala	Tyr
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Glu	Phe	Met	Ser	Gln	Ala	Phe	Ser	Leu	Tyr	Glu	Asp	Glu	Ile	Ser	Asp
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Ser	Lys	Ala	Gln	Leu	Ala	Ala	Ile		Leu	Ile	Ile	Gly		Phe	Glu
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Arg	Met		Cys	Phe	Ser	Glu		Asn	His	Glu	Pro		Arg	Thr	Gln
	_	595				_	600	_	_	_		605	<b>~</b> `	<b>-</b> 3	•
Cys		Leu	Ala	Ala	Ser		Leu	Leu	Lys	Lys		Asp	GIN	GIY	Arg
	610			_	m1-	615		m	C	03	620	B	σ.p. ~~	7	T
Ala	GIu	Hls	Leu	Cys	Inr	ser	ren	rrp	ser	Gly	Arg	ASI	TIIL	usp	rλa

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635
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Lys Ala Leu Lys Ile Ala Asn Gln Cys Met Asp Pro Ser Leu Gln Val
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Gln Leu Phe Ile Glu Ile Leu Asn Arg Tyr Ile Tyr Phe Tyr Glu Lys
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                            680
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                        695
Ile Arg Glu Asp Leu Pro Asn Leu Glu Ser Ser Glu Glu Thr Glu Gln
                                        715
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Ile Leu Cys Glu Phe Glu Thr Leu Tyr Lys Ala Phe Ser Asn Cys Ser
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Leu Pro Gln Gly Trp Lys Met Asn Ser Thr Pro Ser Gly Glu Trp Phe
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Thr Phe Tyr Leu Val Asn Gln Gly Val Cys Val Pro Arg Asn Cys Arg
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Lys Cys Pro Arg Thr Tyr Arg Leu Leu Gly Ser Leu Arg Thr Cys Ile
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His Leu Gly Leu Lys Thr Pro Asn Gly Cys Glu Leu Val Val Gly Gly
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Glu Pro Gln Cys Trp Ala Glu Gly Arg Cys Leu Leu Phe Asp Asp Ser
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Phe Leu His Ala Ala Phe His Glu Gly Ser Ala Glu Asp Gly Pro Arg
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Tyr Leu Phe Ser Leu Pro Ile Lys Glu Ser Glu Ile Ile Asp Phe Phe
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Leu Gly Ala Ser Leu Lys Asp Glu Val Leu Lys Ile Met Pro Val Gln
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Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala Phe Val Ala
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Ile Gly Asp Tyr Asn Gly His Val Gly Leu Gly Val Lys Cys Ser Lys
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His Thr Val Pro Cys Lys Val Thr Gly Arg Cys Gly Ser Val Leu Val
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Arg Leu Ile Pro Ala Pro Arg Gly Thr Gly Ile Val Ser Ala Pro Val
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Pro Lys Lys Leu Leu Met Met Ala Gly Ile Asp Asp Cys Tyr Thr Ser
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Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
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J	530					535				1	540	1			
Acn		Ser	Gln	Dro	Thr		Δτα	Gln	TIA	Ara		Ser	Ser	Pro	Glu
545		J-12			550	•	9			555					560
	Gln	Δτα	Ť.e.r	Ser		T.e.11	Yen	T.em	Thr		Asp	Pro	Glu	Met	
~r9		.~~y	Leu	565	J C L	are u	<b>7311</b>	عا تابير	570					575	
											_		_	-	
Dro	Pro	Pra	Lare	D~~	DYC	2~~	50~	Cve	Ser	Ala	Len	Ala -	Ara	His	A.I.A

585

580

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Phe Cys Lys Ala Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala
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Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His
Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly
Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val
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GIN	290	ire	Leu	ASI	nis	295	Inr	Leu	PIO	Asp	Leu 300	Cys	Arg	reu	ALA
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Pho	Tan	355	Val	Cve	Glv	Sar	360	T.011	Va 1	Ara	Leu	365	T.e.11	Ser	ᡥ
FIIC	370	Ly 3	Vul	Cys	Ory	375	014	200	•	••••	380			•••	o, o
Ser	His	Phe	Leu	Asn	Glu	Thr	Cys	Leu	Glu	Val	Ile	Ser	Glu	Met	Cys
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Pro	Asn	Leu	Gln		Leu	Asn	Leu	Ser		Cys	Asp	Lys	Leu		Pro
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Gly	Trp	Cys		Thr	Leu	Gln	Ser		Thr	Gly	Cys	Phe		Arg	Leu
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neu	$\Delta \gamma c \sigma$														
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Gln Val His Pro Asn Ser Ser Leu Ala Gln Lys Trp Cys Tyr Ile His
Trp Glu Gln Thr Cys Ile Pro Thr Pro Arg His Val Thr Thr Gly Thr
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Ala Asn Glu Leu Cys Pro Gly Asn Ser Phe Thr Pro Ser Ser Cys Ser
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Thr Arg Cys Cys Cys Ser Ser Asp Pro Cys Cys Glu Glu Trp Asp Ser
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Trp Ser Lys Leu Val Phe Leu Phe Cys Ile Asn Glu Lys Asn Pro
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250

Leu Ser Asn Val Ala Gly Tyr Lys Ala Ile Tyr His Asp Leu Glu Gln
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Arg Gln Ala Cys Val Trp Thr Ser Ala Gly Ala Ala Ala Leu Arg Leu
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240
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Val Met Met Glu Gln Ile Arg Pro Trp His Ser Arg Met Lys Arg Arg
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105

100

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Cys Met Glu Gly Ile Cys Lys Pro Asp Pro Arg Ile Tyr Lys Leu Cys
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Leu Glu Gln Leu Gly Leu Gln Pro Ser Glu Ser Ile Phe Leu Asp Asp
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Leu Gly Thr Asn Leu Lys Glu Ala Ala Arg Leu Gly Ile His Thr Ile
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Pro	GIn	Asp	Leu		Pro	Thr	Ala	Thr		Ser	Ser	Met	Ala		Phe
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Glu	Δla	Pro		Cvs	Pro	T.e.u	Δla		Ser	Δεπ	T.e.11	Glv		Ser	Ara
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Len	Glv		Met	Val	Pro	Val		Tvr	Ara	Lvs	Tle		Cvs	Δsn	Pro
200	370					375		-1-	****	<i></i> , <i></i>	380	7114	<b>-1</b>	r.o.p	110
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Dro	Dro	435	750	Thr	Ser	λl 5	440	17-1	ca-	7~~	ת ז ת	445	17-1	T ov	7.55
PLO	450	GIU	ASD	TILL	SEL	455	Gru	vai	261	ALG	460	1111	vai	Leu	Asp
Leu		Glv	Asn	Ala	Arg		Asp	Lvs	Glv	Ser		Ser	Glu	Asp	Cvs
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C3	530	אן א	7	Dwa	<i>α</i> 1	535	N	D	17-3	<b>~</b> 3	540	C	***	~1··	3
545	vəħ	ALA	wry	FIO	Glu 550	GIU	AT.G	FIO	val	555	Asp	ser	urs	OTÅ	560
	Ile	Ara	Pro	Len	Arg	Lve	G] n	Val	Glii		T.em	Phe	Aen	ጥኮ~	
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Tyr	Ala	Lys	Ala		Gly	Ile	Ser	Glu		Val	Lys	Val	Pro		Ser
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Pro Gly Lys Glu Arg Lys Gln Asn Pro Lys His Gln Asn Glu Leu Arg
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D==	» T -	C1	660	777	The	ui c	Phe			מות	Dha	Cyc		) en	Lare
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T ALL		GÍV	Thr	Glu	GIn		Leu	ጥኒ/ም	21 =	T.e.11		Val	T.e.11	Larg	Asn
865	Val	GLY	1111	Giu	870	O.L.y	<u> </u>	- 7 -	nia	875	7311	V CL 2	Deu	Lys	880
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Cys	Ser		Ile	His	Pne	Thr	Asn		ser	IIe	Leu			Inr	Asn
	D	995	<b>~</b> 3	T1 -	N ===	We t	1000		m	mъ	•	1005		nh-	T
Lys	Lue	Tyr	GIU	TTE	Asp	met	Lys	GIN	ıyr	Thr	геп	GIU	GIU	Fue	Leu

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Val Ala Gly Phe Val His His Gly Thr Val Leu Asp Cys Glu Glu Lys
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Thr Arg Val Leu Arg Gly His Thr Asp Tyr Ile His Cys Leu Ala Leu
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Arg Val Lys Ala Lys Gln Lys Pro Leu Ile Ser Asn Ser His Thr Asp
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Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser
Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn
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Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp
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Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn
His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala
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Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met
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Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln
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Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp
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Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr
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Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser
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Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu
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Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro Glu
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Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val Asp Gly
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Lys Gly Asn Val Leu Ala Ala Arg Tyr Pro Cys Asp Val Glu Asp Cys
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Glu Ala Leu Gly Ala Leu Val Cys Arg Val Gln Leu Gly Pro Tyr Gln
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Asn Phe Val Ser Lys Glu Glu Phe Gln Ala Val Glu Lys Lys Leu Val
Glu Glu Lys Ala Ala His Ala Lys Thr Lys Val Leu Leu Ala Lys Glu
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Glu Glu Lys Leu Gln Phe Ala Leu Gly Glu Val Glu Val Leu Ser Lys
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Gln Leu Glu Lys Glu Lys Leu Ala Phe Glu Lys Ala Leu Ser Ser Val
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Lys Ser Lys Val Leu Gln Glu Ser Ser Lys Lys Asp Gln Leu Ile Thr
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Lys Cys Asn Glu Ile Glu Ser His Ile Ile Lys Gln Glu Asp Ile Leu
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Asn Gly Lys Glu Asn Glu Ile Lys Glu Leu Gln Gln Val Ile Ser Gln
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Gln Lys Gln Ile Phe Ser Pro Pro Pro Ala Gly Ser Val Ala Gly Ile
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Thr Cys Leu Thr Ser Gly Ser Arg Ser Ser Arg Lys Ala Thr Trp Pro
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Arg Cys Trp Thr Arg Ser Ile Arg Lys Pro Gln Gly His Val Arg Pro
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Ala Ala Thr Ser Ile Pro Gly Lys Asn Lys Met Ala Ala Ala Phe Leu
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Phe Ser Gly Cys Asn Pro Gln Pro Leu Pro Ser Leu Leu Trp Glu Ser
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Pro Ala Ser Ser Pro Cys Tyr Phe Pro Pro Ser Trp Ile Val Val Gly
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Val His Lys Val Gly Ala Cys Ser Leu Gly Glu Glu Leu Gly Leu Cys
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Cys Leu Val Gly Thr Thr Ala Ser Phe Gly Tyr Leu Ile Pro Ser Tyr
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Leu Val Asn
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Thr Val Tyr Tyr Pro Gln Val His Leu Gly Thr Ile Ser Gly Ala Gly
Met Val Arg Pro Thr Ser Val Thr Pro Gly Leu Phe Gln Val Leu Lys
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Ala Val Tyr Phe Ala Cys Tyr Ser Lys Ala Lys Glu Gln Phe Asn Gly
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Ile Phe Val Pro Asn Ser Asn Ile Val His Leu Phe Ser Ala Gly Ser
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Asp Asp Leu Ser Asn Ala Ala Arg Glu Leu Arg Val Leu Ile Asp Asp
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Ser Gln Ser Ile Ile Phe Ile Asn Leu Asp Ser His Arg Asn Val Met
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Ile Arg Leu Asn Leu Gln Leu Thr Met Gly Thr Phe Ser Leu Ser Leu
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70

65

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Gly Ser Gly Leu Ile Trp Arg Arg Leu Leu Ser Phe Leu Gly Arg Gln
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                                                 125
Leu Glu Ala Pro Leu Pro Pro Met Met Ala Ser Leu Pro Lys Lys Thr
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Gln Arg Ser Lys Gln Ala Leu Gln Glu Leu Thr Gln Asn Gln Val Val
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Leu Asp Ser Ser Arg Cys Leu Met Gln Gln Gly Ile Lys Ala Gly Asp
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Ala Leu Trp Leu Arg Phe Lys Tyr Tyr Ser Phe Phe Asp Leu Asp Pro
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Ile Phe Arg Pro Arg Lys Leu Thr Leu Lys Gly Tyr Arg Gln His Trp
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Val Val Phe Lys Glu Thr Thr Leu Ser Tyr Tyr Lys Ser Gln Asp Glu
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Ala Pro Gly Asp Pro Ile Gln Gln Leu Asn Leu Lys Gly Cys Glu Val
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Val Pro Ser Pro Glu Gly Met Ser Glu Ile Tyr Leu Arg Cys Gln Asp
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Glu Gln Gln Tyr Ala Arg Trp Met Ala Gly Cys Arg Leu Ala Ser Lys
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Arg Tyr Tyr Lys Glu Thr Ser Gly Leu Met Leu Asp Val Gly Pro Tyr
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Asp Phe Glu Asn Ile Glu Ser Pro Leu Asn Glu Arg Asp Ser Ser Ala
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Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Gln Ile Pro Glu
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Asn Gly Leu Thr Ser Pro Leu Thr Glu Pro Val Val Leu Glu Gly
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His Thr Lys Arg Val Gly Ile Ile Ala Trp His Pro Thr Ala Arg Asn
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Val Leu Leu Ser Ala Gly Cys Asp Asn Val Val Leu Ile Trp Asn Val
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Cys Lys Asp Lys Ser Val Arg Ile Ile Asp Pro Arg Arg Gly Thr Leu
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# What is claimed is:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amina acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is any integer 1-3161, or the complement thereof.

- 2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2n wherein n is any integer 1-3161, or the complement thereof.
- 3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ I) NO: 2n, wherein n is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of S) ID NO: 2n.
- 4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes: polypeptide comprising the amino acid sequence selected from the group consisting of SEQ Il NO: 2n, wherein n is any integer 1-3161.
- 5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprise the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein *i* any integer 1-3161, or the complement thereof.
- 6. An oligonucleotide less than 100 nucleotides in length and comprising at least contiguous nucleotides selected from the group consisting of SEQ ID NO:2n-1, wherein n is a integer 1-3161, or the complement thereof.
  - 7. A vector comprising the nucleic acid molecule of claim 1.

- 8. The vector of claim 7, wherein said vector is an expression vector.
- 9 A host cell comprising the isolated nucleic acid molecule of claim 1.
- 10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
- 11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
  - 12. An antibody that selectively binds to the polypeptide of claim 10.
- 13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:
  - a) the nucleic acid of claim 1;
  - b) the polypeptide of claim 10; and
  - c) the antibody of claim 12; and a pharmaceutically acceptable carrier.
- 14. A kit comprising in one or more containers, a therapeutically or prophylactically effective amount of the pharmaceutical composition of claim 13.
- 15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.
- 16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said

compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

- 17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe or primer bound to the nucleic acid molecule of claim 1 is present in the sample.
- 18. A method for modulating the activity of the polypeptide of claim 10, the method comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptid
- 19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected fro the group consisting of:
  - a) the nucleic acid of claim 1;
  - b) the polypeptide of claim 10; and
  - c) the antibody of claim 12.
- 20. A method for screening for a modulator of activity or of latency or predispositio to an ORFX-associated disorder, said method comprising:
  - a) contacting a test compound with the polypeptide of claim 10; and
- b) determining if said test compound binds to said polypeptide, wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.
- 21. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:
  - a) administering a test compound to a test subject at an increased risk ORFX-associated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;

- b) measuring expression the activity of said protein in said test subject;
- c) measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and
- d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predisposition to an ORFX-associated disorder.
- 22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.
- 23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:
  - a) measuring the amount of the polypeptide in a sample from said subject; and
  - b) comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

- 24. The method of claim 23, wherein said subject is a human.
- 25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:
  - a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and
  - b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the corsample indicates the presence of or predisposition to said disease in said subject.

- 26. The method of claim 25, wherein said subject is a human.
- 27. A method of treating or preventing a pathological condition associated with at ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.
  - 28. The method of claim 27, wherein said subject is a human.
- 29. A method of treating or preventing a pathological condition associated with ar ORFX-associated disorder in a subject, the method comprising administering to said subject nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said patholog condition.
  - 30. The method of claim 29, wherein said subject is a human.
- 31. A method of treating or preventing a pathological condition associated with ar ORFX-associated disorder in a subject, the method comprising administering to said subject 1 antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological conditio
  - 32. The method of claim 31, wherein said subject is a human.

## (19) World Intellectual Property Organization International Bureau



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#### (43) International Publication Date 5 October 2000 (05.10.2000)

# (10) International Publication Number WO 00/58473 A3

- (51) International Patent Classification7: C12N 15/12. C07K 14/47, 16/18, G01N 33/566, C12Q 1/68, C12N 15/11, 15/62, A01K 67/027, A61K 38/00
- Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US).
- (21) International Application Number: PCT/US00/08621
- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (22) International Filing Date: 31 March 2000 (31.03.2000)
- (81) Designated States (national): AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,

RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA,

(25) Filing Language:

- (26) Publication Language:

English

English

(30) Priority Data:

60/127,607	31 March 1999 (31.03.1999)	US
60/127,636	2 April 1999 (02.04.1999)	US
60/127,728	5 April 1999 (05.04.1999)	US
09/540,763	30 March 2000 (30.03.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	60/127,607 (CIP)
Filed on	31 March 1999 (31.03.1999)
US	60/127,636 (CIP)
Filed on	2 April 1999 (02.04.1999)
US	60/127,728 (CIP)
Filed on	5 April 1999 (05.04.1999)
US	09/540,763 (CIP)
Filed on	30 March 2000 (30.03.2000)

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- (72) Inventors; and
- (75) Inventors/Applicants (for US only): SHIMKETS.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

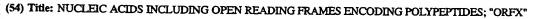
#### Published:

With international search report.

UG, US, UZ, VN, YU, ZA, ZW.

- Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.
- (88) Date of publication of the international search report: 25 January 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



(57) Abstract: The present invention provides open reading frames encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.

## INTERNATIONAL SEARCH REPORT

Internal Application No PCT/US 00/08621

IPC 7	SIFICATION OF SUBJECT MATTER C12N15/12 C07K14/47 C0 C12N15/11 C12N15/62 A0			C12Q1/68
According	to International Patent Classification (IPC) or to both national	al classification and	IPC	
	S SEARCHED			
Minimum of IPC 7	documentation searched (classification system followed by c C12N C07K G01N A01K A61K		ois)	
Document	ation searched other than minimum documentation to the ext	tent that such docu	ments are included in the	fields searched
	data base consulted during the international search (name of S, EMBASE, MEDLINE, CAB Data, PA		•	•
C. DOCUM	ENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where appropriate,	of the relevant pas	sages	Relevant to claim No.
A	COLE S.T.: "Deciphering the Mycobacterium tuberculosis f complete genome sequence."  NATURE, vol. 393, 11 June 1998 (1998 XP002144873 sequence  LAMERDIN J.E.: "Sequence and 3.5 Mb contig in human 19p13 a serine protease gene cluste EMEST DATABASE ENTRY, 8 February 1999 (1999-02-08) sequence	rom the -06-11), alysis of .3 container."	a ing	
X Furthe	er documents are listed in the continuation of box C.	P	atent family members are	listed in annex.
A document consider earlier do filing data which is citation of document other me document are that	t which may throw doubts on priority claim(s) or cited to establish the publication date of another or other special reason (as specified) t referring to an oral disclosure, use, exhibition or	or prictical circled invention of the cannot cannot involve cannot documents in the "%" documents of the cannot ca	ent of particular relevance to be considered novel or ce an inventive step when to ent of particular relevance to be considered to involve ent is combined with one , such combination being and.  ent member of the same por mailing of the international	at with the application but or theory underlying the ; the claimed invention cannot be considered to the document is taken alone ; the claimed invention an inventive step when the or more other such docu- obvious to a person skilled
	illing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tet. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		ix, R	

# INTERNATIONAL SEARCH REPORT

Internat' | Application No PCT/US 00/08621

		PCT/US 00/08621		
	on) DOCUMENTS CONSIDERED TO BE RELEVANT			
Zalayury C	citation of document, with indication, where appropriate, of the relevant passages		Relevant to claim No.	
	M.D. ADAMS ET AL.: "The genome sequence of Drosophila melanogaster."  SCIENCE, vol. 287, 24 March 2000 (2000-03-24), pages 2185-2195, XP002144875  the whole document		Relevant to claim No.	

# INTERNATIONAL SEARCH REPORT

ional application No. PCT/US 00/08621

Box I	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)	-
This Inte	ernational Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:	
1. X	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:	
	Although claims 27 to 32 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.	
2.	Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:	
·		
	Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).	
Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)	-
This Inter	national Searching Authority found multiple inventions in this international application, as follows:	-
	see additional sheet	
1. A	as all required additional search fees were timely paid by the applicant, this International Search Report covers all earchable claims.	
2. A	s all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment fany additional fee.	
3. A	s only some of the required additional search fees were timely paid by the applicant, this International Search Report overs only those claims for which fees were paid, specifically claims Nos.:	
	o required additional search fees were timely paid by the applicant. Consequently, this International Search Report is stricted to the invention first mentioned in the claims; it is covered by claims Nos.:  Laims 1 to 32 partially	
Remark on	Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.	
	·	

#### FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim: 1 to 32 partially

Isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from a group consisting of SEQ ID NO 2n wherein n is 1, oligonucleotides less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides from the above sequence, polypeptides encoded by said nucleotides, antibodies that bind to said polypeptide, pharmaceutical composition comprising said polypeptide and methods of detection, screening, therapeutic uses involving said polypeptide.

#### 2. Claim : .

Inventions 2 to 3161

claims 1 to 32 partially:

Isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from a group consisting of SEQ ID NO 2n wherein n is 2 to 3161, oligonucleotides less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides from the above sequence, polypeptides encoded by said nucleotides, antibodies that bind to said polypeptide, pharmaceutical composition comprising said polypeptide and methods of detection, screening, therapeutic uses involving said polypeptide.

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